CE GPCR 19.2

GenCore version 5.1.8

OM protein - protein search, using sw model

Run on: May 8, 2006, 09:27:07 ; Search time 231 Seconds
(without alignments)
1212.531 Million cell updates/sec

Title: US-10-650-467-105
Perfect score: 2074
Sequence: 1 MVSSAATISTISTTTTPSTI.....QLHDLLPTSTHSDRCAGNSF 397

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2074	100.0	397	2	Q9N4R5_CAEEL	Q9n4r5 caenorhabdi
2	1899	91.6	433	2	Q6F3C9_CAEEL	Q6f3c9 caenorhabdi
3	1768.5	85.3	444	2	Q625Z7_CAEBR	Q625z7 caenorhabdi
4	607.5	29.3	450	2	Q23305_CAEEL	Q23305 caenorhabdi
5	529	25.5	600	2	Q9VW75_DROME	Q9vw75 drosophila
6	518.5	25.0	375	2	Q629B2_CAEBR	Q629b2 caenorhabdi
7	514	24.8	468	2	O62062_CAEEL	O62062 caenorhabdi
8	495.5	23.9	470	2	Q7Q0B9_ANOGA	Q7q0b9 anopheles g
9	487.5	23.5	453	2	Q618Q8_CAEBR	Q618q8 caenorhabdi
10	485.5	23.4	457	2	Q18534_CAEEL	Q18534 caenorhabdi
11	462	22.3	430	2	Q8I0L4_CAEEL	Q8i0l4 caenorhabdi
12	461.5	22.3	365	2	Q9XXU4_CAEEL	Q9xxu4 caenorhabdi
13	461	22.2	362	2	Q6EUU1_CAEEL	Q6euu1 caenorhabdi
14	460.5	22.2	387	2	Q22188_CAEEL	Q22188 caenorhabdi
15	458	22.1	402	2	Q20275_CAEEL	Q20275 caenorhabdi
16	456.5	22.0	404	2	Q611A4_CAEBR	Q611a4 caenorhabdi
17	433	20.9	266	2	Q61W82_CAEBR	Q61w82 caenorhabdi
18	432	20.8	492	2	Q6V1R1_SCHMA	Q6v1r1 schistosoma
19	421.5	20.3	402	2	Q964E5_DUGTI	Q964e5 dugesia tig
20	390.5	18.8	375	2	O57463_BRARE	O57463 brachydanio
21	386	18.6	370	1	GPR10_HUMAN	P49683 homo sapien
22	386	18.6	370	2	Q5VXR9_HUMAN	Q5vxr9 homo sapien
23	386	18.6	370	2	Q502U8_HUMAN	Q502u8 homo sapien
24	385.5	18.6	370	2	Q6VMN6_MOUSE	Q6vmn6 mus musculu
25	384	18.5	377	2	Q8QGM3_CHICK	Q8qgm3 gallus gall
26	383	18.5	377	2	Q61SJ7_CAEBR	Q61sj7 caenorhabdi
27	382	18.4	376	2	P90745_CAEEL	P90745 caenorhabdi
28	379	18.3	481	2	Q7KFF8_DROME	Q7kff8 drosophila
29	379	18.3	485	2	Q9VNM1_DROME	Q9vnm1 drosophila
30	378	18.2	316	2	Q60UD5_CAEBR	Q60ud5 caenorhabdi
31	378	18.2	485	2	Q8SZ35_DROME	Q8sz35 drosophila
32	373.5	18.0	370	1	GPR10_RAT	Q64121 rattus norv
33	373.5	18.0	374	2	Q9YHX1_GADMO	Q9yhx1 gadus morhu
34	372	17.9	400	2	Q7PQN7_ANOGA	Q7pqn7 anopheles g
35	372	17.9	425	2	Q5QGM5_ANOGA	Q5qgm5 anopheles g
36	371	17.9	339	2	Q4SRZ3_TETNG	Q4srz3 tetraodon n
37	369.5	17.8	396	2	Q501I5_FUGRU	Q501i5 fugu rubrip
38	368	17.7	434	2	Q59E83_CAEEL	Q59e83 caenorhabdi
39	367.5	17.7	427	2	Q9N324_CAEEL	Q9n324 caenorhabdi
40	367.5	17.7	438	2	Q615K7_CAEBR	Q615k7 caenorhabdi
41	366.5	17.7	370	2	Q4EW11_BOVIN	Q4ew11 bos taurus
42	364.5	17.6	371	1	NPY6R_RABIT	P79217 oryctolagus
43	363	17.5	372	2	Q6PR57_BRARE	Q6pr57 brachydanio
44	361.5	17.4	354	2	Q501I3_FUGRU	Q501i3 fugu rubrip
45	360.5	17.4	369	2	Q501I4_FUGRU	Q501i4 fugu rubrip

ALIGNMENTS

RESULT 1
Q9N4R5_CAEEL
ID Q9N4R5_CAEEL PRELIMINARY; PRT; 397 AA.
AC Q9N4R5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Y58G8A.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; AC006808; AAF60815.3; -; Genomic_DNA.
DR Ensembl; Y58G8A.4; Caenorhabditis elegans.
DR WormBase; WBGene00021983; Y58G8A.4.
DR WormPep; Y58G8A.4a; CE33345.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Complete proteome; G-protein coupled receptor; Hypothetical protein;
KW Receptor; Transducer; Transmembrane.
SQ SEQUENCE 397 AA; 44536 MW; 092E3CAC4E765F81 CRC64;

Query Match 100.0%; Score 2074; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 3.2e-149;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MVSSAATISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MVSSAATISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF 60

Qy         61 LYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKD 120

Qy        121 WAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 WAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIV 180
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11 Dec. 1998

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Qy        181 STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM 240

Qy        241 AVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 300

Qy        301 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKIL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKIL 360

Qy        361 NSTEGSKKAGGSGLRGIQLHDLLPTSTHSDRCAGNSF 397
              |||||||||||||||||||||||||||||||||||||
Db        361 NSTEGSKKAGGSGLRGIQLHDLLPTSTHSDRCAGNSF 397


RESULT 2
Q6F3C9_CAEEL
ID   Q6F3C9_CAEEL PRELIMINARY;      PRT;   433 AA.
AC   Q6F3C9;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=Y58G8A.4;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RG   The C. elegans sequencing consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR   EMBL; AC006808; AAT68889.1; -; Genomic_DNA.
DR   Ensembl; Y58G8A.4; Caenorhabditis elegans.
DR   WormBase; WBGene00021983; Y58G8A.4.
DR   WormPep; Y58G8A.4b; CE36962.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Complete proteome; G-protein coupled receptor; Hypothetical protein;
KW   Receptor; Transducer; Transmembrane.
SQ   SEQUENCE   433 AA;  48919 MW;  57D033F5FDDA70F5 CRC64;

  Query Match             91.6%;  Score 1899;  DB 2;  Length 433;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-136;
  Matches  364;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MVSSAATISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MVSSAATISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF 60

Qy         61 LYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKD 120

Qy        121 WAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 WAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIV 180

Qy        181 STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM 240

Qy        241 AVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 300

Qy        301 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKIL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKIL 360

Qy        361 NSTE 364
              ||||
Db        361 NSTE 364


RESULT 3
Q625Z7_CAEBR
ID   Q625Z7_CAEBR PRELIMINARY;      PRT;   444 AA.
AC   Q625Z7;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein CBG01072.
GN   Name=CBG01072;
OS   Caenorhabditis briggsae.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6238;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RG   The C.briggsae Sequencing Consortium;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR   EMBL; CAAC01000007; CAE58004.1; -; Genomic_DNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Hypothetical protein; Receptor;
KW   Transducer; Transmembrane.
SQ   SEQUENCE   444 AA;  50089 MW;  B1794980E7DFC16A CRC64;

  Query Match             85.3%;  Score 1768.5;  DB 2;  Length 444;
  Best Local Similarity   91.0%;  Pred. No. 5.7e-126;
  Matches  342;  Conservative   11;  Mismatches   10;  Indels   13;  Gaps    2;

Qy          2 VSSAATISTIST--------TTTPSTISNVI-----TSHSNNGSCIQIAEAIAAQGIDDI 48
              ::|:| :  |||        ||:|:  |:||     ||  |||:|||||||||||||||
Db          1 MTSSAVLHPISTTISSPTISTTSPTIHSHVITTTQSTSSQNNGTCIQIAEAIAAQGIDDI 60

Qy         49 TVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTA 108
              |||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TVDFYIRTIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTA 120

Qy        109 IPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIR 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIR 180

Qy        169 QALAITFLIWIVSTLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYG 228
              ||| || |||||||||||||||||:|||||||||||||||||||||||||||||||||||
Db        181 QALGITSLIWIVSTLINLPYLMSFEHVEGSFYVQPGETPYCGHFCDEANWQSENSRKIYG 240

Qy        229 TTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYIL 288
              ||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db        241 TTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRNDATSRKKKVNYIL 300
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Qy        289 IAMVVTFIGCWLPLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLT 348
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        301 IAMVVTFIGCWLPLTLLNLVKDFKKEPEWLKRQPFFWAIVAHVIAMSLVVWNPLLFFWLT 360

Qy        349 RKQKRSGLSKILNSTE 364
              ||||||||||||||||
Db        361 RKQKRSGLSKILNSTE 376


RESULT 4
Q23305_CAEEL
ID   Q23305_CAEEL PRELIMINARY;      PRT;   450 AA.
AC   Q23305;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein ZC412.1.
GN   ORFNames=ZC412.1;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RG   The C. elegans sequencing consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR   EMBL; Z78067; CAB01528.2; -; Genomic_DNA.
DR   PIR; T27559; T27559.
DR   Ensembl; ZC412.1; Caenorhabditis elegans.
DR   WormBase; WBGene00013883; ZC412.1.
DR   WormPep; ZC412.1; CE35920.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000611; NPY_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01012; NRPEPTIDEYR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Complete proteome; G-protein coupled receptor; Hypothetical protein;
KW   Receptor; Transducer; Transmembrane.
SQ   SEQUENCE   450 AA;  51887 MW;  42860ED8E26BF5C1 CRC64;

  Query Match             29.3%;  Score 607.5;  DB 2;  Length 450;
  Best Local Similarity   35.3%;  Pred. No. 8.5e-38;
  Matches  119;  Conservative   76;  Mismatches  111;  Indels   31;  Gaps    7;

Qy         33 CIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNV 92
              || :   :  |  :| || | :|  :: ||  : ::|: ||| :: ::   |:| |  |:
Db          9 CIDVNAIL--QQFNDWTVLFEVRLGYSVLYFLILIIGLVGNGLLITSILMRKKL-SVANI 65

Qy         93 FLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLD 152
              ||:||  :||:|  ||:|:||  |  | | || :|| |||   : || ::|||| |::|
Db         66 FLINLAVSDLLLCITAVPITPVLAFMKRWIFGIIMCKLVPTCQAFSVLISSWSLCYIAID 125

Qy        153 KFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDGSFYVQPGET------ 206
              ::  |  | ::| | | |  :    |:|: | : |           :| |  :|
Db        126 RYRSIVTPLREPWSDRHARWLLMFTWVVAFLASYPL----------YYSQNLKTMVIENV 175

Qy        207 PYCGHFCDEANWQSENSRKI-YGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQF 265
              || || | ||||:   |: | |:::::| ::|  ::::||  |||||  | ::
Db        176 TLCGDFCGEFNWQSDEISKLTYTTSLLIIQLIIPAIIMSFCYLMILQKVQTDWLVDEGSM 235

Qy        266 CQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEW-------- 317
                 ||  |::    ||::| |:|| ||: |: || ||: :|| :|      |:
Db        236 ---LTAAQQAQTAVRKRRVMYVLILMVIVFMACWFPLSAVNLFRDLGMRFEFCQTVYKVL 292

Qy        318 LKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRS 354
              :  | :|  :| ||||||: :||||:|:||:::: :|:
Db        293 MMDQMYFKLLNVHVIAMTSIVWNPVLYFWMSKRHRRA 329


RESULT 5
Q9VW75_DROME
ID   Q9VW75_DROME PRELIMINARY;      PRT;   600 AA.
AC   Q9VW75; Q9VW74;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   CG7395-PA (GH23382p) (Neuropeptide F-like receptor).
GN   Name=NPFR76F; ORFNames=CG7395;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
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RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RG   Berkeley Drosophila Genome Project;
RA   Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA   Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA   Yu C., Rubin G.;
RT   "Drosophila melanogaster release 4 sequence.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RG   FlyBase;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Berkeley;
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA   Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA   Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
RA   Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Canton-S; TISSUE=Head;
RA   Feng G., Reale V., Chatwin H., Kennedy K., Venard Re., Ericsson C.,
RA   Yu K., Evans P.D., Hall L.M.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR   EMBL; AE003514; AAF49074.2; -; Genomic_DNA.
DR   EMBL; AY051588; AAK93012.1; -; mRNA.
DR   EMBL; AY192578; AAO39845.1; -; mRNA.
DR   Ensembl; CG7395; Drosophila melanogaster.
DR   FlyBase; FBgn0036934; CG7395.
DR   FlyBase; FBgn0036934; NPFR76F.
DR   GO; GO:0008188; F:neuropeptide receptor activity; IDA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000611; NPY_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01012; NRPEPTIDEYR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Neuropeptide; Receptor; Transducer;
KW   Transmembrane.
SQ   SEQUENCE   600 AA;  66579 MW;  EE63BEF821BDA14B CRC64;

  Query Match             25.5%;  Score 529;  DB 2;  Length 600;
  Best Local Similarity   30.5%;  Pred. No. 1.1e-31;
  Matches  136;  Conservative   76;  Mismatches  154;  Indels   80;  Gaps   12;

Qy          6 ATISTISTTTPST---------ISNVITSHSNNGSCIQIAEAIAAQGID---DITVDFY 53
              | :| :|| || |:          :|     | :: |:   |    :||   |     |  : :
Db          2 ANLSWLSTITTTSSSISTSQLPLVSTTNWSLTSPGTTSAILADVAASDEDRSGGIIHNQF 61

Qy         54 IRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTP 113
              ::  |  ||  :||||:|||  | : | ||: :|:  |:|: ||  :|::|    |:| ||
Db         62 VQIFFYVLYATVFVLGVFGNVLVCYVVLRNRAMQTVTNIFITNLALSDILLCVLAVPFTP 121

Qy        114 WYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAI 173
               |    ||||  :|||| :  ||:::: :||:|::|::  |  |    : :   : |
Db        122 LYTFMGRWAFGRSLCHLVSFAQGCSIYISTLTLTSIAIDRYFVIIYPFHPRMKLSTCIGI 181

Qy        174 TFLIWIVSTLINLPYLMSFE--------------------HVDGSFYVQPG-------- 204
              ||::: |  :|| |  :                      ::||| |
Db        182 IVSIWVIALLATVPYGMYMKMTNELVNGTQTGNETLVEATLMLNGSFVAQGSGFIEAPDS 241

Qy        205 -----------------ETPYCGHPCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYC 246
                              | ||   :|:| || ||  ||::|     ||||:|  :|: |
Db        242 TSATQAYMQVMTAGSTGPEMPYVRVYCEE-NWPSEQYRKVFGAITTTLQFVLPFFIISIC 300

Qy        247 YFKILQKVSKDMIIQNAQFCQSLTQKQRSDA-TSRKKKVNYILIAMVVTFIGCWLPLTLL 305
              |  |  |::     | |:        :| :|   |||: | :|||||  |   |||: ::
Db        301 YVWISVKLN-----QRARAKPGSKSSRREEADRDRKKRTNRMLIAMVAVFGLSWLPINVV 355

Qy        306 NLVKDF-KKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLT---RKQKRSGL----- 356
              |:  ||  |  ||        ||:   || ||||   :|| |: ||    ||: :  |
Db        356 NIFDDFDDKSNEWRFYILFFFV--AHSIAMSSTCYNPFLYAWLNENFRKEFKHVLPCFNP 413

Qy        357 --SKILNSTEGSKKAGGSGLRGIQLH 380
                : |:| | |  ::  :   | :||
Db        414 SNNNIINITRGYNRSDRNTC-GPRLH 438


RESULT 6
Q629B2_CAEBR
ID   Q629B2_CAEBR PRELIMINARY;      PRT;   375 AA.
AC   Q629B2;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein CBG00112 (Fragment).
GN   Name=CBG00112;
OS   Caenorhabditis briggsae.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6238;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RG   The C.briggsae Sequencing Consortium;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CAAC01000002; CAE57235.1; -; Genomic_DNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000611; NPY_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01012; NRPEPTIDEYR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Hypothetical protein; Receptor;
KW   Transducer; Transmembrane.
FT   NON_TER       1      1
FT   NON_TER     375    375
SQ   SEQUENCE   375 AA;  42616 MW;  341E2844A0156E9A CRC64;
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  Query Match           25.0%;  Score 518.5;  DB 2;  Length 375;
  Best Local Similarity  33.3%;  Pred. No. 4.1e-31;
  Matches  113;  Conservative   68;  Mismatches  113;  Indels   45;  Gaps    7;

Qy         46 DDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILV 105
              :|::  :||  || |||  :   || ||  |: |: ||| ||:  |:|:|:|  :|:::
Db         18 EDMSTRWYIMLIFAFLYLIIIAAGIIGNTCVILAITRNKALQTVPNLFILSLSCSDIVVC 77

Qy        106 FTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPV 165
               |:  :||  |  |:| || |:| : |      |:  ::::|||||:|::: |  | ::|:
Db         78 CTSATITPITAFKKEWIFGEVLCRVAPFIAGISLCYSTFTLTAISIDRYILIRFPMRKPI 137

Qy        166 SIRQALAITFLIWIVSTLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANW-QSENSR 224
              |  ||| :  ||   :  |  | :  |:   | |        :|| :| | ||  :|: |
Db        138 SHYQALGVIALICAFAATITSPIM--FKQRLGEF------ENFCGLYCTE-NWGANESQR 188

Qy        225 KIYGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSD-------- 276
              ||||  :| || |:|: :|   |  |  |: : ||:: |       :||::|
Db        189 KIYGAALMFLQLVIPLTIIIISYTAISLKIGQSMILKGA-------KKQKTDNWEIELSD 241

Qy        277 ----ATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEWLKRQPFFWAINAHVI 332
                  |  |::: | :|| ||| |   |:     |:::|::  |: :| | : :  | | |
Db        242 QQRMAVKRRQRTNRMLIGMVVAFACSWIWSVTFNILRDYEYLPDLIKNQEYIFGIATHCI 301

Qy        333 AMSLVVWNPLLFF----------------WLTRKQKRSG 355
              ||:  ||||||:                || |:    |
Db        302 AMTSTVWNPLLYAVLNLQLRAAFIDLMPQWLRRRLNLDG 340


RESULT 7
O62062_CAEEL
ID   O62062_CAEEL PRELIMINARY;      PRT;   468 AA.
AC   O62062;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein C16D6.2.
GN   ORFNames=C16D6.2;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RG   The C. elegans sequencing consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR   EMBL; Z81472; CAB03888.2; -; Genomic_DNA.
DR   PIR; T19340; T19340.
DR   Ensembl; C16D6.2; Caenorhabditis elegans.
DR   WormBase; WBGene00007635; C16D6.2.
DR   WormPep; C16D6.2; CE37317.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000611; NPY_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01012; NRPEPTIDEYR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Complete proteome; G-protein coupled receptor; Hypothetical protein;
KW   Receptor; Transducer; Transmembrane.
SQ   SEQUENCE   468 AA;  52773 MW;  2A0F72C78EE353D5 CRC64;

  Query Match           24.8%;  Score 514;  DB 2;  Length 468;
  Best Local Similarity  31.3%;  Pred. No. 1.1e-30;
  Matches  114;  Conservative   74;  Mismatches  128;  Indels   48;  Gaps    9;

Qy         29 NNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQS 88
              |   |: :   :     :|::  :||  :| |||  :   || ||  |: |: ||| ||:
Db          2 NGSDCLNLNSELWLYR-EDLSSRWYIMLVFAFLYLIIIAAGIIGNSCVILAITRNKSLQT 60

Qy         89 ARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTA 148
                |:|:|:|  :|:::  |:  :||  |  |:| ||  :| : |      |:  ::::|||
Db         61 VPNLFILSLSCSDIVVCCTSATITPITAFKKEWIFGEALCRIAPFIAGISLCFSTFTLTA 120

Qy        149 ISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDGSFYVQPGETPY 208
              ||:|::: |  | ::|::  ||: :  :|   :  |  | :  |:   | |        :
Db        121 ISIDRYILIRFPMRKPITHYQAVGVIAIICAFAATITSPIM--FKQKLGEF------ENF 172

Qy        209 CGHFCDEANW-QSENSRKIYGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQFCQ 267
              || :| | ||  :|: |||||  :| || |:|: :|   |  |  |: : ||:: |
Db        173 CGQYCTE-NWGANESQRKIYGAALMFLQLVIPLTIIIISYTAISLKIGQSMILKGA---- 227

Qy        268 SLTQKQRSD------------ATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEP 315
                 :||::|            |  |::: | :|| ||| |   |:     |:::|::  |
Db        228 ---KKQKTDNWEMELSDQQRIAVKRRQRTNRMLIGMVVAFACSWIWSVTFNILRDYEYLP 284

Qy        316 EWLKRQPFFWAINAHVIAMSLVVWNPLLF----------------FWLTRKQKRSG--LS 357
              | :| | : : |  | |||:  ||||||:                || |    |   |
Db        285 ELIKTQEYIFGIATHCIAMTSTVWNPLLYAVLNLQLRAAFIDLMPHWLRRHLNLEGDNSS 344

Qy        358 KILN 361
               :||
Db        345 PLLN 348


RESULT 8
Q7Q0B9_ANOGA
ID   Q7Q0B9_ANOGA PRELIMINARY;      PRT;   470 AA.
AC   Q7Q0B9;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ENSANGP00000011806 (Fragment).
GN   Name=GPRNPY3; ORFNames=ENSANGG00000009317;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC   Anophelinae; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RT   "Anopheles gambiae re-annotation.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAAB01008986; EAA00213.1; -; Genomic_DNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000611; NPY_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01012; NRPEPTIDEYR.
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DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT   NON_TER     470    470
SQ   SEQUENCE   470 AA;  51957 MW;  B99EBDE9B505DC4D CRC64;

  Query Match             23.9%;  Score 495.5;  DB 2;  Length 470;
  Best Local Similarity   27.3%;  Pred. No. 2.9e-29;
  Matches  121;  Conservative   84;  Mismatches  158;  Indels   81;  Gaps   13;

Qy          5 AATISTISTTTTPSTISNVITSHSN-------NGSCIQIAEAIAAQGIDDITVDF----- 52
              | |::| :|:|:|: ::::: |:          : :  |  :      ::|:
Db         14 AVTVAT-ATSTSPAAMASLVLDHTELPLAGTIPPAALMPARVLLPSNATNLTLTLEELLR 72

Qy         53 -------------------YIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNV 92
                              :: :|  ||  :||||:|||  | : | ||| :|:  |:
Db         73 PNSSTVAPPNGDNDIIFSNKLVQIVFCVLYSSIFVLGVFGNVLVCYVVFRNKAMQTVTNL 132

Qy         93 FLLNLIPTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLD 152
              |: ||  :|::|   |:| || |   : | || ::|| |||:  |||:::: :||:|::|
Db        133 FITNLALSDILLCVLAVPFTPSYTFMRRWVFGKLLCHTVPLAQGCSVYISTLTLTSIAID 192

Qy        153 KFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPY----------LMSFEHVDGSFYVQ 202
              :|  |  |    : :   : |  |||  : :: :||          |   ::  |
Db        193 RFFVIIYPFHPRMKLSTCITIIVLIWSFAIMVTMPYGLYMKLHGVALNGTDNATGPL--- 249

Qy        203 PGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQN 262
                ||      |  | ||  || :     :||||:|  :: :||  :  :::     :
Db        250 -SSAMYC-----EELWPSEEMRKTFSIVTSILQFVLPFIIMAFCYICVSIRLNDRARTKP 303

Qy        263 AQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKE-PEWLKRQ 321
                | | ::       |||: | :||:||  |   |||| ::|:  ||  :   |
Db        304 G----SKTSRREEADRDRKKRTNRMLISMVAIFGISWLPLNVVNMCNDFNSDINSWRFYN 359

Qy        322 PFFWAINAHVIAMSLVVWNPLLFFWLT---RKQKRSGL-----SKILNSTEGSKKAGGSG 373
                |:   ||: |||   :|| |: ||     ||: :  |      |:     | |  :  | |
Db        360 LIFFI--AHLTAMSSTCYNPFLYAWLNDNFRKEFKQVLPCFDPSRGRAGTVGGNRGAGGG 417

Qy        374 LRGIQLHDLLPTSTHSDR-CAGNS 396
                |               |:| | ||:
Db        418 WR------------SERTCNGNN 428


RESULT 9
Q618Q8_CAEBR
ID   Q618Q8_CAEBR PRELIMINARY;      PRT;   453 AA.
AC   Q618Q8;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein CBG14540.
GN   Name=CBG14540;
OS   Caenorhabditis briggsae.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6238;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RG   The C.briggsae Sequencing Consortium;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR   EMBL; CAAC01000068; CAE68647.1; -; Genomic_DNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000611; NPY_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01012; NRPEPTIDEYR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Hypothetical protein; Receptor;
KW   Transducer; Transmembrane.
SQ   SEQUENCE   453 AA;  52101 MW;  38A7F401B1054A3D CRC64;

  Query Match             23.5%;  Score 487.5;  DB 2;  Length 453;
  Best Local Similarity   30.5%;  Pred. No. 1.1e-28;
  Matches  118;  Conservative   77;  Mismatches  115;  Indels   77;  Gaps   11;

Qy         58 PTFLYGPLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIPTDLILVFTAIPVTPWYAM 117
              |  :| ||| ||:|||  :::      | | | :|:|:||| :|:::   ::|:||   :
Db         29 FLCVYIPLFFLGLFGNVTLIYVTCSYKALLSVQNIFILNLAASDIMMCILSLPITPITNV 88

Qy        118 TKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLI 177
              |:| ||:::|||:|      |:|| ::|| ||:||::: :  |   |:| | |   | |:
Db         89 YKNWYFGNLLCHLIPCIQGISIFVCTFSLGAIALDRYILVVRPHTTPLSQRGAFLTTILL 148

Qy        178 WIVSTLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFV 237
              ||:| :: |||  : : :: :     |   ||:|| |  |:|  ||: |   ||| |||
Db        149 WILSFVVTLPYAFNMQMIEYT------EEHICGYFCTE-KWESAKSRRAYTMIVMLAQFV 201

Qy        238 VPMAVITYCY---FKILQKVSKDMIIQNAQFCQSL-----------------------T 270
              :| ||: :||   | :| | ::  | :  :   :|
Db        202 LPFAVMAFCYSNIFSVLSKRAQTKIRKMVERTSALESSCAFPSHGLEQYENELNEFLDKQ 261

Qy        271 QKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEWLKRQPFF------ 324
              :|::     : ::   ||: ||| |   |||  :::|: ::       : | ||
Db        262 EKEKQRVVLQNRRTTSILVTMVVWFGITWLPHNVVSLIIEYD------ETQSFFRLFGRD 315

Qy        325 -----WAIN--AHVIAMSLVVWNPLLFFWLT---------------RKQKR----SGL-- 356
                  : :|   | |||| :| ||:|: ||                 ||  |    : |
Db        316 DYDISYLLNLFTHSIAMSNIVVNPVLYAWLNPSFRQLVIKTYFGDRRKSDRIINQTSLYK 375

Qy        357 SKILN---STEGSKKAGGSGLRGIQLH 380
                |:||   :: |  | | | |:  :|:
Db        376 QKMLNEAKNSNGRMKNGNSCLKERELN 402


RESULT 10
Q18534_CAEEL
ID   Q18534_CAEEL PRELIMINARY;      PRT;   457 AA.
AC   Q18534;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Neuropeptide receptor family protein 1.
GN   Name=npr-1; ORFNames=C39E6.6;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RG   The C. elegans sequencing consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR   EMBL; U49944; AAA93419.1; -; Genomic_DNA.
DR   PIR; T29741; T29741.
DR   Ensembl; C39E6.6; Caenorhabditis elegans.
DR   WormBase; WBGene00003807; npr-1.
DR   WormPep; C39E6.6; CE06941.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
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DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000611; NPY_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01012; NRPEPTIDEYR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Complete proteome; G-protein coupled receptor; Neuropeptide; Receptor;
KW   Transducer; Transmembrane.
SQ   SEQUENCE   457 AA;  52464 MW;  6EB950A91BB10BE8 CRC64;

  Query Match             23.4%;  Score 485.5;  DB 2;  Length 457;
  Best Local Similarity   30.8%;  Pred. No. 1.6e-28;
  Matches  117;  Conservative   69;  Mismatches  117;  Indels   77;  Gaps   10;

Qy         58 FTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAM 117
              |  :| ||| ||:|||  :::    :| | | :|:|:|||  :| ::   ::|:||   :
Db         29 FLTVYLFLFFLGLFGNVTLIYVTCSHKALLSVQNIFILNLAASDCMMCILSLPITPITNV 88

Qy        118 TKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLI 177
              |:| ||:::|||:|     |:|| ::|| ||:||::: :   |   |:| | |   | |:
Db         89 YKNWYFGNLLCHLIPCIQGISIFVCTFSLGAIALDRYILVVRPHSTPLSQRGAFLTTVLL 148

Qy        178 WIVSTLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFV 237
              ||:| :: ||| : : :: :      |   ||:|| |  |:|  ||: |   ||| |||
Db        149 WILSFVVTLPYAFNMQMIEYT------EERICGYFCTE-KWESAKSRRAYTMIVMLAQFV 201

Qy        238 VPMAVITYCYFKILQKVSK-------DMIIQNA--------------QFCQSLT------ 270
              || ||: :||  |:  :||        |: : :              |:  |
Db        202 VPFAVMAFCYANIVSVLSKRAQTKIRKMVERTSALESSCAFPSHGLEQYENELNEFLDKQ 261

Qy        271 QKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEWLKRQPFF------ 324
              :|::     : ::   ||: ||| |   |||  :::|: ::        | ||
Db        262 EKEKQRVVLQNRRTTSILVTMVVWFGITWLPHNVISLIIEYD------DTQSFFRLYGRD 315

Qy        325 -----WAIN--AHVIAMSLVVWNPLLFFWL----------TRKQKRSGLSKILNST---- 363
                  : :|   | ||||  | ||:|: ||          |    |    :|:| |
Db        316 DYDISYLLNLFTHSIAMSNNVLNPVLYAWLNPSFRQLVIKTYFGDRRKSDRIINQTSVYK 375

Qy        364 ----------EGSKKAGGSG 373
                       |  | || |
Db        376 TKIVHDTKHLNGRAKIGGGG 395


RESULT 11
Q8I0L4_CAEEL
ID   Q8I0L4_CAEEL PRELIMINARY;      PRT;   430 AA.
AC   Q8I0L4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein npr-2.
GN   Name=npr-2; ORFNames=T05A1.1, T05A1.1a;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RG   The C. elegans sequencing consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR   EMBL; Z68216; CAD59147.1; -; Genomic_DNA.
DR   EMBL; Z68219; CAD59155.1; -; Genomic_DNA.
DR   EMBL; Z68219; CAD59147.1; JOINED; Genomic_DNA.
DR   EMBL; Z68216; CAD59155.1; JOINED; Genomic_DNA.
DR   Ensembl; T05A1.1; Caenorhabditis elegans.
DR   WormBase; WBGene00003808; npr-2.
DR   WormPep; T05A1.1a; CE32924.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000611; NPY_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01012; NRPEPTIDEYR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Complete proteome; G-protein coupled receptor; Hypothetical protein;
KW   Receptor; Transducer; Transmembrane.
SQ   SEQUENCE   430 AA;  49138 MW;  4B0E8890C94CB9E2 CRC64;

  Query Match             22.3%;  Score 462;  DB 2;  Length 430;
  Best Local Similarity   28.4%;  Pred. No. 9.1e-27;
  Matches  112;  Conservative   83;  Mismatches  130;  Indels   70;  Gaps   10;

Qy         23 VITSHSNNGSCIQIAEAIAAQGID---DITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWA 79
              :|  ||:     |   |    : ||   |:| :  :   |: ||  :|:||| ||  ||:
Db         36 LIQLHSS--QMINETEETCDRYIDKHPDMTNEPTVLVTFSLLYLHIFLLGILGNSAVLYL 93

Qy         80 VARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSV 139
                 ::::|:: :|:|:|||  :::::  |::|:|    : | | | | :| |:||    |:
Db         94 TMKHRQLQTVQNIFILNLCASNVLMCLTSLPITFITNVYKQWFFSSPVCKLIPLVQGASI 153

Qy        140 FVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPY--LMSFEHVDG 197
              ||:::||:||:||::  :  | || :| | |: |  |||::| :: :||   |  | ::|
Db        154 FVSTFSLSAIALDRYNLVVRPHKQKLSSRSAMMIALLIWVISVVVCMPYGWYMDVEKLNG 213

Qy        198 SFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYCYFKI------- 250
                    || :| | :|     || |   |:: ||: | | : :||: |
Db        214 ----------LCGEYCSE-HWPLAEVRKGYTFLVLITQFLPFFATMAFCYYNIFSRLRQR 262

Qy        251 ----LQKVS-KDMIIQNAQFC--------------QSLTQKQRSDATSRKKKVNYILIA 290
                  |:|:| :  :::|:  |                |  |||    :::::   ||
Db        263 VETKLKKLSERSQLLENSTTCGTTNHIVSINAEAVQNGLENKQRLAVLAQQRRTTTILSC 322

Qy        291 MVVTFIGCWLPLTLLNLVKDFKKEPEWLKRQPFFW---------------AINAHVIAM 334
              ||: |   |||  :: |: ::          ||:              :: ||:|:|
Db        323 MVLLFAFTWLPHNVVTLMIEY---------DGFFFHSDETSATSTDHTYIVSMTAHLISM 373

Qy        335 SLVVWNPLLFFWLTRKQKRSGLSKILNSTEGSKKA 369
                | || |: ||     |   :  :   ::  | |
Db        374 LTNVTNPFLYAWLNPMFKEMLIKTLRGGSKSPKPA 408


RESULT 12
Q9XXU4_CAEEL
ID   Q9XXU4_CAEEL PRELIMINARY;      PRT;   365 AA.
AC   Q9XXU4;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein C53C7.1a.
GN   ORFNames=C53C7.1, C53C7.1a;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RG   The C. elegans sequencing consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
CC   -!- INTERACTION:
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CC       O44820:F52C6.3; NbExp=1; IntAct=EBI-318084, EBI-318098;
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR   EMBL; AL008868; CAA15513.1; -; Genomic_DNA.
DR   PIR; T20184; T20184.
DR   HSSP; P02699; 1L9H.
DR   IntAct; Q9XXU4; -.
DR   Ensembl; C53C7.1; Caenorhabditis elegans.
DR   WormBase; WBGene00008278; C53C7.1.
DR   WormPep; C53C7.1a; CE19767.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000611; NPY_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01012; NRPEPTIDEYR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Complete proteome; G-protein coupled receptor; Hypothetical protein;
KW   Receptor; Transducer; Transmembrane.
SQ   SEQUENCE   365 AA;  40860 MW;  5DB21F7EBF5B89AF CRC64;

  Query Match             22.3%;  Score 461.5;  DB 2;  Length 365;
  Best Local Similarity   30.9%;  Pred. No. 8.4e-27;
  Matches  110;  Conservative   79;  Mismatches  138;  Indels   29;  Gaps    8;

Qy         28 SNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQ 87
              |::  || |  |   |   |:|:     :|  :|  : |:|: ||  |: :| | | ||
Db          2 SSSNHCIDI-RAYLWQTKHDLTLHPIPIAILATIYTIIVVVGVTGNLLVVMSVMRFKVLQ 60

Qy         88 SARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLT 147
              | ||:|:::|  :|: :   :  |||  | :| | ||  :|||:||    ::  :: :||
Db         61 SVRNMFIVSLSVSDIFVAIVSGSVTPITAFSKVWLFGGPLCHLLPLLQGTALSFSTLTLT 120

Qy        148 AISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPY-----LMSFEHVDGSFYVQ 202
              ||::|::: |  |||:|:   ||| :      :|  :::|      || | :
Db        121 AIAIDRYILICHPTKEPIRKDQALKMISFNSAISVGLSVPLFMKQELMQFRN-------- 172

Qy        203 PGETPYCGHFCDEANWQSE-NSRKIYGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQ 261
                 ||| :| | ||  :   | :||| | ::||| |:  ||:|| |  |: : : ::
Db        173 -----YCGEYCSE-NWGPDAYLRSVYGTVVFIIQFVFPLITITFCYASISIKLRRGVFVR 226

Qy        262 NAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEWLKRQ 321
               :|  : |  : |   | |: : | :|| | |||   |||    | ::|:   |  :  |
Db        227 GSQ--KELMSEARRQLTQRRLRTNRMLIIMTVTFALSWLPSVGFNFLRDYSALPGIIDSQ 284

Qy        322 PFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKILNSTEGSKKAGGSGLRGI 377
               : : |  | |:|: |: || |: :   :  |:  : :|:: : :      |:| :
Db        285 DYLFGIIFHCISMTSVIVNPFLYGY-CNEHFRAAFAALLDTVKAA-----CGMRRV 334


RESULT 13
Q6EUU1_CAEEL
ID   Q6EUU1_CAEEL PRELIMINARY;      PRT;   362 AA.
AC   Q6EUU1;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein C53C7.1b.
GN   ORFNames=C53C7.1, C53C7.1B;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RG   The C. elegans sequencing consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR   EMBL; AL008868; CAH04724.1; -; Genomic_DNA.
DR   Ensembl; C53C7.1; Caenorhabditis elegans.
DR   WormBase; WBGene00008278; C53C7.1.
DR   WormPep; C53C7.1b; CE36989.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000611; NPY_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01012; NRPEPTIDEYR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Complete proteome; G-protein coupled receptor; Hypothetical protein;
KW   Receptor; Transducer; Transmembrane.
SQ   SEQUENCE   362 AA;  40577 MW;  D81B10D5CF877651 CRC64;

  Query Match             22.2%;  Score 461;  DB 2;  Length 362;
  Best Local Similarity   31.3%;  Pred. No. 9.1e-27;
  Matches  108;  Conservative   77;  Mismatches  136;  Indels   24;  Gaps    7;

Qy         28 SNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQ 87
              |::  || |  |   |   |:|:     :|  :|  : |:|: ||  |: :| | | ||
Db          2 SSSNHCIDI-RAYLWQTKHDLTLHPIPIAILATIYTIIVVVGVTGNLLVVMSVMRFKVLQ 60

Qy         88 SARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLT 147
              | ||:|:::|  :|: :   :  |||  | :| | ||  :|||:||    ::  :: :||
Db         61 SVRNMFIVSLSVSDIFVAIVSGSVTPITAFSKVWLFGGPLCHLLPLLQGTALSFSTLTLT 120

Qy        148 AISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPY-----LMSFEHVDGSFYVQ 202
              ||::|::: |  |||:|:   ||| :      :|  :::|      || | :
Db        121 AIAIDRYILICHPTKEPIRKDQALKMISFNSAISVGLSVPLFMKQELMQFRN-------- 172

Qy        203 PGETPYCGHFCDEANWQSE-NSRKIYGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQ 261
                 ||| :| | ||  :   | :||| | ::||| |:  ||:|| |  |: : : ::
Db        173 -----YCGEYCSE-NWGPDAYLRSVYGTVVFIIQFVFPLITITFCYASISIKLRRGVFVR 226

Qy        262 NAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEWLKRQ 321
               :|  : |  : |   | |: : | :|| | |||   |||    | ::|:   |  :  |
Db        227 GSQ--KELMSEARRQLTQRRLRTNRMLIIMTVTFALSWLPSVGFNFLRDYSALPGIIDSQ 284

Qy        322 PFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKILNSTEGS 366
               : : |  | |:|: |: || |: :   :  |:  : :|:: : :
Db        285 DYLFGIIFHCISMTSVIVNPFLYGY-CNEHFRAAFAALLDTVKAA 328


RESULT 14
Q22188_CAEEL
ID   Q22188_CAEEL PRELIMINARY;      PRT;   387 AA.
AC   Q22188;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein npr-2.
GN   Name=npr-2; ORFNames=T05A1.1, T05A1.1B;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RG   The C. elegans sequencing consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
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RT   investigating biology.";
RL   Science 282:2012-2018(1998).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR   EMBL; Z68219; CAA92481.2; -; Genomic_DNA.
DR   PIR; T24487; T24487.
DR   Ensembl; T05A1.1; Caenorhabditis elegans.
DR   WormBase; WBGene00003808; npr-2.
DR   WormPep; T05A1.1b; CE32925.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000611; NPY_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01012; NRPEPTIDEYR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Complete proteome; G-protein coupled receptor; Hypothetical protein;
KW   Receptor; Transducer; Transmembrane.
SQ   SEQUENCE   387 AA;  44128 MW;  195C02A8A65772FE CRC64;

  Query Match             22.2%;  Score 460.5;  DB 2;  Length 387;
  Best Local Similarity   28.5%;  Pred. No. 1.1e-26;
  Matches  105;  Conservative   80;  Mismatches  118;  Indels   65;  Gaps    8;

Qy         47 DITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVF 106
              |:| :  :   |: ||  :|:||| ||  ||:   ::::||: :|:|:|||  :::::
Db         18 DMTNEPTVLVTFSLLLYLHIFLLGILGNSAVLYLTMKHRQLQTVQNIFILNLCASNVLMCL 77

Qy        107 TAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVS 166
              |::|:|    : | | | | :| |:||    |:||:::||:||:||::  :  | || :|
Db         78 TSLPITFITNVYKQWPFSSPVCKLIPLVQGASIFVSTFSLSAIALDRYNLVVRPHKQKLS 137

Qy        167 IRQALAITFLIWIVSTLINLPY--LMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSR 224
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Db        138 SRSAMMIALLIWVISVVVCMPYGWYMDVEKLNG----------LCGEYCSE-HWPLAEVR 186

Qy        225 KIYGTTVMLLQFVVPMAVITYCYFKI-----------LQKVS-KDMIIQNAQFC------ 266
              | |   |:: ||: | | : :||: |           |:|:| :  :::|:  |
Db        187 KGYTFLVLITQFLFPFATMAFCYYNIFSRLRQRVETKLKKLSERSQLLENSTTCGTTNHI 246

Qy        267 ---------QSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEW 317
                      |  |||    :::::   ||  ||: |   |||  :: |: ::
Db        247 VSINAEAVQNGLENKQRLAVLAQQRRTTTILSCMVLLFAFTWLPHNVVTLMIEY------ 300

Qy        318 LKRQPFFW----------------AINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKILN 361
                 ||:                 :: ||:|:|   | || |: ||     |   :  :
Db        301 ---DGFFFHSDETSATSTDHTYIVSMTAHLISMLTNVTNPFLYAWLNPMFKEMLIKTLRG 357

Qy        362 STEGSKKA 369
               ::  | |
Db        358 GSKSPKPA 365


RESULT 15
Q20275_CAEEL
ID   Q20275_CAEEL PRELIMINARY;      PRT;   402 AA.
AC   Q20275;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein F41E7.3.
GN   ORFNames=F41E7.3;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RG   The C. elegans sequencing consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR   EMBL; Z68106; CAA92126.2; -; Genomic_DNA.
DR   PIR; T22076; T22076.
DR   Ensembl; F41E7.3; Caenorhabditis elegans.
DR   WormBase; WBGene00009619; F41E7.3.
DR   WormPep; F41E7.3; CE31509.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000611; NPY_receptor.
DR   InterPro; IPR000408; Reg_chr_condens.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01012; NRPEPTIDEYR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR   PROSITE; PS00626; RCC1_2; UNKNOWN_1.
KW   Complete proteome; G-protein coupled receptor; Hypothetical protein;
KW   Receptor; Transducer; Transmembrane.
SQ   SEQUENCE   402 AA;  46285 MW;  7DE92DA66E9AC523 CRC64;

  Query Match             22.1%;  Score 458;  DB 2;  Length 402;
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              ::|:|   ||||  |       ||   ::                  | |  |  :|  :|
Db          8 SVSSILNETTPSYQST--CKIKNNPMEME----------------YFRPFFISMYCAVF 48

Qy         67 VLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSV 126
              ::   ||  |:: |  |||:|:  |:|: ||  :|::: ||:: :|| |      | ||
Db         49 LVASSGNFLVVYVVMTNKRMQTITNIFITNLAVSDIMVNFTSLWLTPTYTSIGHWIFGGG 108

Qy        127 MCHLVPLSNSCSVFVTSWSLTAISLDKF---------LHINDPTKQPVSIRQALAITFLI 177
              :|| :||    |:|:::|:||||::|::         ::|||     :|:|  |:   ||
Db        109 LCHGLPLFQGTSIFISTWTLTAIAIDRYIVIVHNSSNININD----RMSMRSCLSFIVLI 164

Qy        178 WIVSTLINLPYL----MSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVML 233
              |: | |:  ||      ::: |     | :            | | :| :   | |:|  ||:
Db        165 WLCSLLLVTPYAINMKLNYIHEPCDFLI-----------CSE-DWSNAEFRSIFGIVVMI 212

Qy        234 LQFVVPMAVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVV 293
              |||::|  :|    | ||         :  |::  ||:|:: :||   |||::  :|| |||
Db        213 LQFILPFVLIAISYIKI-------WLFLNSR--QSMTER-KSD-IKRKKRLLRMLIVMVV 261

Qy        294 TFIGCWLPLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWL 347
              |  || |  ||| ::| | :  :::    |  :: |:::|:   |||:|: ::
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Job time : 234 secs
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GenCore version 5.1.8

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_ba:*
2: gb_in:*
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5: gb_ov:*
6: gb_pat:*
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8: gb_pr:*
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13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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3	1193	100.0	1500	6	AR408559	AR408559 Sequence
4	1193	100.0	1500	6	AX151254	AX151254 Sequence
5	1109	93.0	1301	6	AR408594	AR408594 Sequence
6	1109	93.0	1301	6	AX151321	AX151321 Sequence
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13	78.8	6.6	1352	6	AR408548	AR408548 Sequence
14	78.8	6.6	1352	6	AX151230	AX151230 Sequence
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16	67.2	5.6	1303	2	AY579078	AY579078 Anopheles
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19	65	5.4	1158	5	AF309091	AF309091 Gallus ga
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22	62.2	5.2	2018	9	S65355	S65355 nonselectiv
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44	60.2	5.0	2504	6	CQ613713	CQ613713 Sequence
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ALIGNMENTS

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LOCUS AR408593 1193 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 104 from patent US 6632621.
ACCESSION AR408593
VERSION AR408593.1 GI:40158833
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1193)
AUTHORS Lowery,D.E., Geary,T.G., Kubiak,T.M. and Larsen,M.J.
TITLE G protein-coupled receptor-like receptors and modulators thereof
JOURNAL Patent: US 6632621-A 104 14-OCT-2003;
Pharmacia & Upjohn Company; Kalamazoo, MI
FEATURES Location/Qualifiers
source 1. .1193
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ORIGIN

Query Match 100.0%; Score 1193; DB 6; Length 1193;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       361 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 420
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DEFINITION  Sequence 104 from Patent WO0138533.
ACCESSION   AX151319
VERSION     AX151319.1  GI:14533456
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lowery,D.E., Geary,T.G., Kubiak,T.M. and Larsen,M.J.
  TITLE     G protein-coupled receptor-like receptors and modulators thereof
  JOURNAL   Patent: WO 0138533-A 104 31-MAY-2001;
            PHARMACIA & UPJOHN COMPANY (US)
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     source          1. .1193
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ORIGIN
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Qy        661 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 720

Qy        721 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 780

Qy        781 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 840

Qy        841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900

Qy        901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960

Qy        961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020

Qy       1021 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1080

Qy       1081 AACTCAACAGAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAGGGATCCAGCTACAC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AACTCAACAGAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAGGGATCCAGCTACAC 1140

Qy       1141 GACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 1193
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Db       1141 GACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 1193


RESULT 3
AR408559
LOCUS       AR408559                1500 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 39 from patent US 6632621.
ACCESSION   AR408559
VERSION     AR408559.1  GI:40158799
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1500)
  AUTHORS   Lowery,D.E., Geary,T.G., Kubiak,T.M. and Larsen,M.J.
  TITLE     G protein-coupled receptor-like receptors and modulators thereof
  JOURNAL   Patent: US 6632621-A 39 14-OCT-2003;
            Pharmacia & Upjohn Company; Kalamazoo, MI
FEATURES             Location/Qualifiers
     source          1. .1500
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 1193;  DB 6;  Length 1500;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1193;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 366

Qy         61 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        367 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 426

Qy        121 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 486

Qy        181 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 546

Qy        241 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 606

Qy        301 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 666

Qy        361 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 726

Qy        421 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC 786

Qy        481 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 846

Qy        541 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC 906

Qy        601 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 966

Qy        661 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 1026

Qy        721 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 1086

Qy        781 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 1146

Qy        841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 1206

Qy        901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 1266

Qy        961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1267 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1326

Qy       1021 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1386

Qy       1081 AACTCAACAGAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAGGGATCCAGCTACAC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 AACTCAACAGAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAGGGATCCAGCTACAC 1446

Qy       1141 GACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 1193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 GACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 1499
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RESULT 4
AX151254
LOCUS       AX151254               1500 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 39 from Patent WO0138533.
ACCESSION   AX151254
VERSION     AX151254.1  GI:14533418
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lowery,D.E., Geary,T.G., Kubiak,T.M. and Larsen,M.J.
  TITLE     G protein-coupled receptor-like receptors and modulators thereof
  JOURNAL   Patent: WO 0138533-A 39 31-MAY-2001;
            PHARMACIA & UPJOHN COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .1500
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             1. .1500
                     /note="unnamed protein product; Clone identifier:
                     CEGPCR19"
                     /codon_start=1
                     /protein_id="CAC42575.1"
                     /db_xref="GI:14533419"
                     /translation="MEIILCFLNYLAHFKAGFEIDLFNFINITIYKKFPFFFHRLKFD
                     RKLDFMINFQNTLFDPPILEKNIFRFSNLKNLKTLKFSTIFLFYGFYACNFLQNNLRC
                     MVSSAATISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIF
                     TFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYA
                     MTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAIT
                     FLIWIVSTLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVM
                     LLQFVVPMAVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIA
                     MVVTFIGCWLPLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLT
                     RKQKRSGLSKILNSTEGSKKAGGSGLRGIQLHDLLPTSTHSDRCAGNSF"
ORIGIN

  Query Match           100.0%;  Score 1193;  DB 6;  Length 1500;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1193;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 366

Qy         61 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 426

Qy        121 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 486

Qy        181 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 546

Qy        241 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 606

Qy        301 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 666

Qy        361 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 726

Qy        421 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC 786

Qy        481 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 540
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Qy        541 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC 906

Qy        601 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 966

Qy        661 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 1026

Qy        721 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 1086

Qy        781 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 1146

Qy        841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 1206

Qy        901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960
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Db       1207 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 1266

Qy        961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020
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Db       1267 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1326

Qy       1021 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1080
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Db       1327 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1386

Qy       1081 AACTCAACAGAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAGGGATCCAGCTACAC 1140
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Db       1387 AACTCAACAGAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAGGGATCCAGCTACAC 1446

Qy       1141 GACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 1193
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Db       1447 GACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 1499


RESULT 5
AR408594
LOCUS       AR408594               1301 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 106 from patent US 6632621.
ACCESSION   AR408594
VERSION     AR408594.1  GI:40158834
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1301)
  AUTHORS   Lowery,D.E., Geary,T.G., Kubiak,T.M. and Larsen,M.J.
  TITLE     G protein-coupled receptor-like receptors and modulators thereof
  JOURNAL   Patent: US 6632621-A 106 14-OCT-2003;
            Pharmacia & Upjohn Company; Kalamazoo, MI
FEATURES             Location/Qualifiers
     source          1. .1301
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ORIGIN
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  Query Match             93.0%;  Score 1109;  DB 6;  Length 1301;
  Best Local Similarity   94.2%;  Pred. No. 0;
  Matches 1193;  Conservative    0;  Mismatches    0;  Indels   74;  Gaps    1;

Qy          1 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 60

Qy         61 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120

Qy        121 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 180

Qy        181 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 240

Qy        241 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 300

Qy        301 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 360

Qy        361 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 420

Qy        421 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        481 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 540

Qy        541 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC 600

Qy        601 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 660

Qy        661 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 720

Qy        721 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 780

Qy        781 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 840

Qy        841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900

Qy        901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960

Qy        961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020
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Db        961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020

Qy       1021 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1080

Qy       1081 AACTCAACAG---------------------------------------------------- 1090
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Db       1081 AACTCAACAGAGATTGTGTCCTCGTTTGCCAGTAGAGTGAGTAACTCGATTCGGCGGTCA 1140

Qy       1091 ------------------------AGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAG 1126
                                       ||||||||||||||||||||||||||||||||||||
Db       1141 ACGTTTCGGAGAAACAATATTGACAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAG 1200

Qy       1127 GGATCCAGCTACACGACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACT 1186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGATCCAGCTACACGACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACT 1260

Qy       1187 CTTTCTA 1193
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Db       1261 CTTTCTA 1267


RESULT 6
AX151321
LOCUS       AX151321               1301 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 106 from Patent WO0138533.
ACCESSION   AX151321
VERSION     AX151321.1  GI:14533458
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lowery,D.E., Geary,T.G., Kubiak,T.M. and Larsen,M.J.
  TITLE     G protein-coupled receptor-like receptors and modulators thereof
  JOURNAL   Patent: WO 0138533-A 106 31-MAY-2001;
            PHARMACIA & UPJOHN COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .1301
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             1. .>1299
                     /note="unnamed protein product; Clone identifier:
                     CEGPCR19.1"
                     /codon_start=1
                     /protein_id="CAC42580.1"
                     /db_xref="GI:14533459"
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                     TKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANW
                     QSENSRKIYGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSD
                     ATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAM
                     SLVVWNPLLFFWLTRKQKRSGLSKILNSTEIVSSFASRVSNSIRRSTFRRNNIDRVRK
                     KQVVLDCEGSSYTTSSRPLLIRTDVQATLSNGSTSTTREML"
ORIGIN

  Query Match             93.0%;  Score 1109;  DB 6;  Length 1301;
  Best Local Similarity   94.2%;  Pred. No. 0;
  Matches 1193;  Conservative    0;  Mismatches    0;  Indels   74;  Gaps    1;

Qy          1 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 60
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Db          1 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 60

Qy         61 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120
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Db         61 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120

Qy        121 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 180
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Db       121 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 180
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Qy       241 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 300
Db       241 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 300
Qy       301 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 360
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Db       361 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 420
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Db       421 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC 480
Qy       481 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 540
Db       481 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 540
Qy       541 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC 600
Db       541 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC 600
Qy       601 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 660
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Qy       661 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 720
Db       661 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 720
Qy       721 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 780
Db       721 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 780
Qy       781 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 840
Db       781 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 840
Qy       841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900
Db       841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900
Qy       901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960
Db       901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960
Qy       961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020
Db       961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020
Qy      1021 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1080
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Qy      1081 AACTCAACAG---------------------------------------------------- 1090
Db      1081 AACTCAACAGAGATTGTGTCCTCGTTTGCCAGTAGAGTGAGTAACTCGATTCGGCGGTCA 1140
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Db      1141 ACGTTTCGGAGAAACAATATTGACAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAG 1200
Qy      1127 GGATCCAGCTACACGACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACT 1186
Db      1201 GGATCCAGCTACACGACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACT 1260
Qy      1187 CTTTCTA 1193
Db      1261 CTTTCTA 1267
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```
RESULT 7
AC006808/c
LOCUS       AC006808               34544 bp    DNA     linear   INV 23-JUN-2005
DEFINITION  Caenorhabditis elegans cosmid Y58G8A, complete sequence.
ACCESSION   AC006808
VERSION     AC006808.1  GI:4263130
KEYWORDS    HTG.
SOURCE      Caenorhabditis elegans
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 34544)
  AUTHORS   .
  CONSRTM   C. elegans Sequencing Consortium
  TITLE     Genome sequence of the nematode C. elegans: a platform for
            investigating biology
  JOURNAL   Science 282 (5396), 2012-2018 (1998)
   PUBMED   9851916
REFERENCE   2  (bases 1 to 34544)
  AUTHORS   Tin-Wollam,A., Graves,T. and Harrison,M.
  TITLE     The sequence of C. elegans cosmid Y58G8A
  JOURNAL   Unpublished (2001)
REFERENCE   3  (bases 1 to 34544)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-FEB-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4  (bases 1 to 34544)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-MAR-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   5  (bases 1 to 34544)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-MAR-2000) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE   6  (bases 1 to 34544)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-NOV-2001) Department of Genetics, Washington
            University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
            Louis, MO 63110, USA
REFERENCE   7  (bases 1 to 34544)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-MAY-2002) Department of Genetics, Washington
            University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
            Louis, MO 63110, USA
REFERENCE   8  (bases 1 to 34544)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JUN-2002) Department of Genetics, Washington
            University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
            Louis, MO 63110, USA
REFERENCE   9  (bases 1 to 34544)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-NOV-2002) Department of Genetics, Washington
            University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
            Louis, MO 63110, USA
REFERENCE   10 (bases 1 to 34544)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-2003) Department of Genetics, Washington
```

University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA
REFERENCE 11 (bases 1 to 34544)
AUTHORS Wilson,R.
TITLE Direct Submission
JOURNAL Submitted (08-JUL-2004) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA
REFERENCE 12 (bases 1 to 34544)
AUTHORS .
CONSRTM WormBase Consortium
TITLE Direct Submission
JOURNAL Submitted (22-SEP-2004) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA
REFERENCE 13 (bases 1 to 34544)
AUTHORS .
CONSRTM WormBase Consortium
TITLE Direct Submission
JOURNAL Submitted (23-JUN-2005) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA
COMMENT Submitted by:
Genome Sequencing Center
Department of Genetics, Washington University
St. Louis , MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
email: submissions@watson.wustl.edu and jes@sanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one m13 subclone.

For a graphical representation of this clone sequence and its analysis see:
http://www.wormbase.org/db/seq/sequence?name=Y58G8A;class=Sequence

NEIGHBORING CLONE INFORMATION

The 5' clone is R02C2, 3100 bp overlap; the 3' clone is F33E11, 200 bp overlap. Actual start of this clone is at base position 20847 of DC2; actual end is at 7365 of T22H9.

NOTES:

Coding seqences below are the result of integration and manual review of the following data : computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (http://www.ddbj.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C. elegans ORFeome cloning project (http://worfdb.dfci.harvard.edu/), similarity to other proteins from BlastX analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers. tRNAs are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).

FEATURES Location/Qualifiers
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/strain="Bristol N2"
/db_xref="taxon:6239"
/chromosome="V"
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gene 2379. .5358
/locus_tag="Y58G8A.2"
CDS join(2379. .2443,2939. .3603,3779. .5358)
/locus_tag="Y58G8A.2"
/standard_name="Y58G8A.2"
/note="contains similarity to Pfam domains PF03372 (Endonuclease/Exonuclease/phosphatase family), PF00078 (Reverse transcriptase (RNA-dependent DNA polymerase))"
/codon_start=1
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Best Local Similarity 82.0%; Pred. No. 2.3e-85;
Matches 436; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

Qy 499 ATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTCTCAACACTGATAAATCTA 558
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Db 21426 ATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTCTCAACACTGATAAATCTA 21367

Qy 559 CCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTACGTTCAGCCCGGAGAAACT 618
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Db      21366 CCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTACGTTCAGCCCGGAGAAACT 21307

Qy        619 CCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGCGAAAATAGTCGAAAGATT 678
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Db      21306 CCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGCGAAAATAGTCGAAAGATT 21247

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Db      21246 TACGGAACTACGGTTATGTTGTTACAGGTGAGCAAAAACACGCTGACCTAACAACCATAA 21187

Qy        703 ------------------------------------------------------------ 702

Db      21186 AAATTTTGCAAACCTAAATTTTTAAAACTTTTGAAATTTTCCTACATACGTCCAAATTTG 21127

Qy        703 CAGTTCGTCGTGCCGATGGCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTG 762
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Db      21126 CAGTTCGTCGTGCCGATGGCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTG 21067

Qy        763 TCAAAAGACATGATCATCCAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGA 822
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Db      21066 TCAAAAGACATGATCATCCAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGA 21007

Qy        823 AGTGATGCGACGTCACGAAAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACA 882
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Db      21006 AGTGATGCGACGTCACGAAAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACA 20947

Qy        883 TTTATCGGGTGTTGGTTGCCTTTAACATTACTCAATTTGGTCAAAGATTTTA 934
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Db      20946 TTTATCGGGTGTTGGTTGCCTTTAACATTACTCAATTTGGTCAAAGATTTTA 20895
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RESULT 8
AC006705/c
LOCUS       AC006705               195349 bp    DNA     linear   HTG 23-FEB-1999
DEFINITION  Caenorhabditis elegans clone Y108G3c, *** SEQUENCING IN PROGRESS
            ***, 2 unordered pieces.
ACCESSION   AC006705
VERSION     AC006705.1  GI:4263233
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      Caenorhabditis elegans
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 195349)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Caehorhabditis elegans clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 195349)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-FEB-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     * NOTE: This is a 'working draft' sequence. It currently
            * consists of 2 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1    52714: contig of 52714 bp in length
            *   52715    52729: gap of unknown length
            *   52730   195349: contig of 142620 bp in length.
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ORIGIN
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  Best Local Similarity   82.0%;  Pred. No. 2.8e-85;
  Matches  436;  Conservative    0;  Mismatches    0;  Indels   96;  Gaps    1;

Qy        499 ATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTCTCAACACTGATAAATCTA 558
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Qy        559 CCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTACGTTCAGCCCGGAGAAACT 618
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Db      27508 CCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTACGTTCAGCCCGGAGAAACT 27449

Qy        619 CCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGCGAAAATAGTCGAAAGATT 678
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27448 CCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGCGAAAATAGTCGAAAGATT 27389

Qy        679 TACGGAACTACGGTTATGTTGTTA---------------------------------- 702
              |||||||||||||||||||||||||
Db      27388 TACGGAACTACGGTTATGTTGTTACAGGTGAGCAAAAACACGCTGACCTAACAACCATAA 27329

Qy        703 ------------------------------------------------------------ 702

Db      27328 AAATTTTGCAAACCTAAATTTTTAAAACTTTTGAAATTTTCCTACATACGTCCAAATTTG 27269

Qy        703 CAGTTCGTCGTGCCGATGGCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTG 762
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27268 CAGTTCGTCGTGCCGATGGCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTG 27209

Qy        763 TCAAAAGACATGATCATCCAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGA 822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27208 TCAAAAGACATGATCATCCAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGA 27149

Qy        823 AGTGATGCGACGTCACGAAAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACA 882
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27148 AGTGATGCGACGTCACGAAAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACA 27089

Qy        883 TTTATCGGGTGTTGGTTGCCTTTAACATTACTCAATTTGGTCAAAGATTTTA 934
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27088 TTTATCGGGTGTTGGTTGCCTTTAACATTACTCAATTTGGTCAAAGATTTTA 27037
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RESULT 9
AR408550
LOCUS       AR408550               1130 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 21 from patent US 6632621.
ACCESSION   AR408550
VERSION     AR408550.1  GI:40158790
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1130)
  AUTHORS   Lowery,D.E., Geary,T.G., Kubiak,T.M. and Larsen,M.J.
  TITLE     G protein-coupled receptor-like receptors and modulators thereof
  JOURNAL   Patent: US 6632621-A 21 14-OCT-2003;
            Pharmacia & Upjohn Company; Kalamazoo, MI
FEATURES             Location/Qualifiers
     source          1. .1130
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
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  Query Match              8.1%;  Score 96.6;  DB 6;  Length 1130;
  Best Local Similarity   47.0%;  Pred. No. 1.2e-16;
  Matches  438;  Conservative    0;  Mismatches  454;  Indels   39;  Gaps    3;

Qy        136 GATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCCTG 195
              || ||| |  |   |   |  |||||     | | | ||  |||| ||||||  | | |
Db         52 GAAGATTTGTCATCAAGGTGGTACATAATGTTAGTGTTTGCATTTCTCTACCTGATAATC 111

Qy        196 TTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAAACAAGCGG 255
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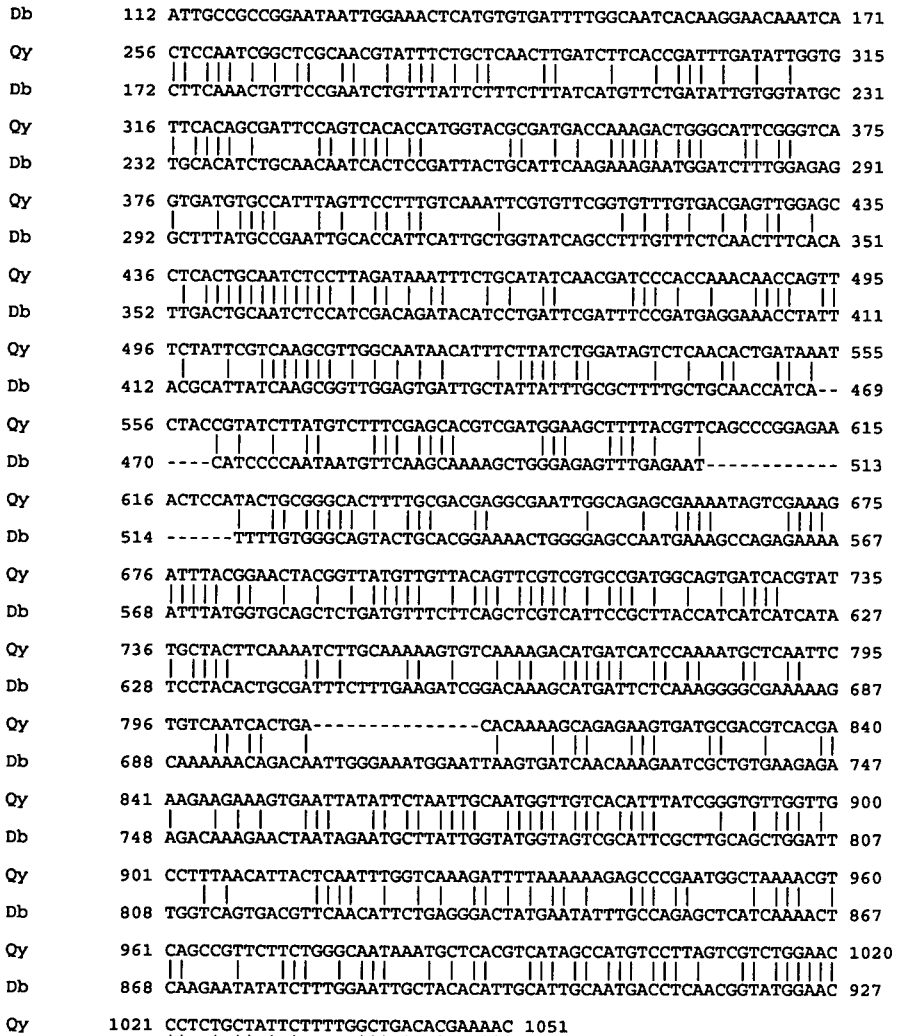

RESULT 10
AX151236
LOCUS AX151236 1130 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 21 from Patent WO0138533.
ACCESSION AX151236
VERSION AX151236.1 GI:14533400
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Lowery,D.E., Geary,T.G., Kubiak,T.M. and Larsen,M.J.
TITLE G protein-coupled receptor-like receptors and modulators thereof
JOURNAL Patent: WO 0138533-A 21 31-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)

FEATURES Location/Qualifiers
source 1. .1130
/organism="Homo sapiens"
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/db_xref="taxon:9606"
CDS 1. .>1128
/note="unnamed protein product; Clone identifier: CEGPCR4"
/codon_start=1
/protein_id="CAC42566.1"
/db_xref="GI:14533401"
/translation="MNGSDCLNLNSELWLYREDLSSRWYIMLVFAFLYLIIIAAGIIG
NSCVILAITRNKSLQTVPNLFILSLSCSDIVVCCTSATITPITAFKKEWIFGEALCRI
APFIAGISLCFSTFTLTAISIDRYILIRFPMRKPITHYQAVGVIAIICAFAATITSPI
MFKQKLGEFENFCGQYCTENWGANESQRKIYGAALMFLQLVIPLTIIIISYTAISLKI
GQSMILKGAKKQKTDNWEMELSDQQRIAVKRRQRTNRMLIGMVVAFACSWIWSVTFNI
LRDYEYLPELIKTQEYIFGIATHCIAMTSTVWNPLLYAVLNLQLRAAFIDLMPHWLRR
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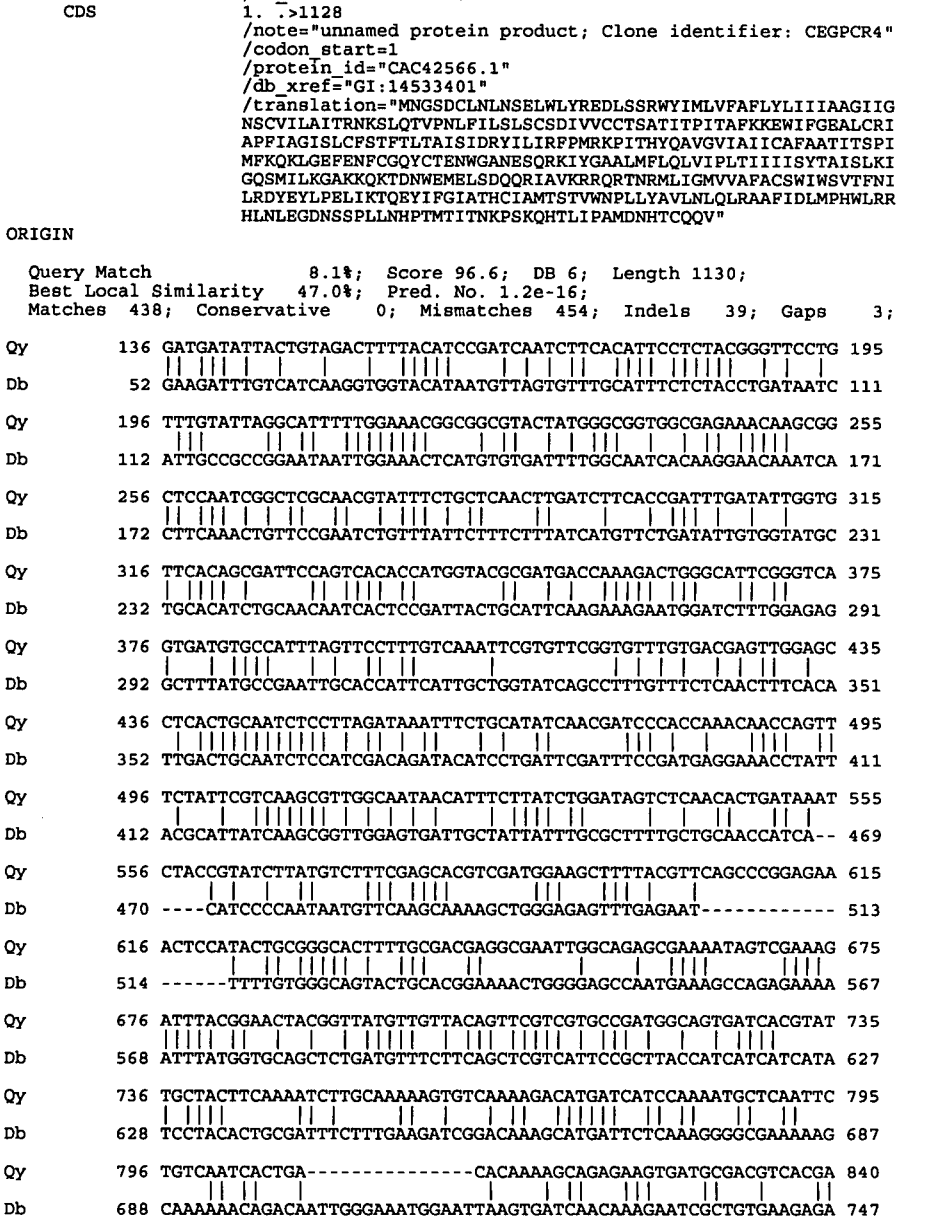
ORIGIN

Query Match 8.1%; Score 96.6; DB 6; Length 1130;
Best Local Similarity 47.0%; Pred. No. 1.2e-16;
Matches 438; Conservative 0; Mismatches 454; Indels 39; Gaps 3;



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Qy        841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900
Db        748 AGACAAAGAACTAATAGAATGCTTATTGGTATGGTAGTCGCATTCGCTTGCAGCTGGATT 807

Qy        901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960
Db        808 TGGTCAGTGACGTTCAACATTCTGAGGGACTATGAATATTTGCCAGAGCTCATCAAAACT 867

Qy        961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020
Db        868 CAAGAATATATCTTTGGAATTGCTACACATTGCATTGCAATGACCTCAACGGTATGGAAC 927

Qy       1021 CCTCTGCTATTCTTTTGGCTGACACGAAAAC 1051
Db        928 CCGTTACTCTACGCAGTGCTCAACCTCCAAC 958


RESULT 11
AR408557
LOCUS       AR408557               1098 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 35 from patent US 6632621.
ACCESSION   AR408557
VERSION     AR408557.1  GI:40158797
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1098)
  AUTHORS   Lowery,D.E., Geary,T.G., Kubiak,T.M. and Larsen,M.J.
  TITLE     G protein-coupled receptor-like receptors and modulators thereof
  JOURNAL   Patent: US 6632621-A 35 14-OCT-2003;
            Pharmacia & Upjohn Company; Kalamazoo, MI
FEATURES             Location/Qualifiers
     source          1. .1098
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             7.0%;  Score 84;  DB 6;  Length 1098;
  Best Local Similarity   50.5%;  Pred. No. 6e-13;
  Matches  204;  Conservative    0;  Mismatches  200;  Indels    0;  Gaps    0;

Qy        167 CAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCG 226
Db         86 CGATTCTTGCAACCATCTACACTATAATTGTCGTAGTTGGCGTAACCGGCAATTTGTTAG 145

Qy        227 TACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCA 286
Db        146 TAGTGATGTCGGTGATGAGGTTCAAAGTTCTTCAATCAGTCAGGAACATGTTCATCGTAT 205

Qy        287 ACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACG 346
Db        206 CTTTGTCAGTTTCTGACATTTTTGTGGCGATTGTTAGTGGTTCAGTAACGCCGATAACCG 265

Qy        347 CGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATT 406
Db        266 CATTCTCTAAAGTTTGGTTATTTGGTGGACCATTGTGTCATTTACTACCTTTGTTACAGG 325

Qy        407 CGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGC 466
Db        326 GTACCGCGTTGAGTTTTTCCACGTTAACGCTCACCGCAATTGCAATTGACAGATATATTC 385

Qy        467 ATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTC 526
Db        386 TCATCTGTCATCCGACGAAAGAACCGATACGCAAAGATCAAGCATTGAAAATGATAAGTT 445

Qy        527 TTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATG 570
Db        446 TCAACAGCGCCATCTCAGTTGGGCTTTCGGTACCATTATTCATG 489


RESULT 12
AX151250
LOCUS       AX151250               1098 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 35 from Patent WO0138533.
ACCESSION   AX151250
VERSION     AX151250.1  GI:14533414
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lowery,D.E., Geary,T.G., Kubiak,T.M. and Larsen,M.J.
  TITLE     G protein-coupled receptor-like receptors and modulators thereof
  JOURNAL   Patent: WO 0138533-A 35 31-MAY-2001;
            PHARMACIA & UPJOHN COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .1098
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
     CDS             1. .1098
                     /note="unnamed protein product; Clone identifier:
                     CEGPCR16"
                     /codon_start=1
                     /protein_id="CAC42573.1"
                     /db_xref="GI:14533415"
                     /translation="MSSSNHCIDIRAYLWQTKHDLTLHPIPIAILATIYTIIVVVGVT
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                     LFMKQELMQFRNYCGEYCSENWGPDAYLRSVYGTVVFIIQFVFPLITITFCYASISIK
                     LRRGVFVRGSQKELMSEARRQLTQRRLRTNRMLIIMTVTFALSWLPSVGFNFLRDYSA
                     LPGIIDSQDYLFGIIFHCISMTSVIVNPFLYGYCNEHFRAAFAALLDTVKAACGMRRV
                     SPGNPACSQLLSTHFESTTRRSVTTTIPSSI"
ORIGIN

  Query Match             7.0%;  Score 84;  DB 6;  Length 1098;
  Best Local Similarity   50.5%;  Pred. No. 6e-13;
  Matches  204;  Conservative    0;  Mismatches  200;  Indels    0;  Gaps    0;

Qy        167 CAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCG 226
Db         86 CGATTCTTGCAACCATCTACACTATAATTGTCGTAGTTGGCGTAACCGGCAATTTGTTAG 145

Qy        227 TACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCA 286
Db        146 TAGTGATGTCGGTGATGAGGTTCAAAGTTCTTCAATCAGTCAGGAACATGTTCATCGTAT 205

Qy        287 ACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACG 346
Db        206 CTTTGTCAGTTTCTGACATTTTTGTGGCGATTGTTAGTGGTTCAGTAACGCCGATAACCG 265

Qy        347 CGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATT 406
Db        266 CATTCTCTAAAGTTTGGTTATTTGGTGGACCATTGTGTCATTTACTACCTTTGTTACAGG 325

Qy        407 CGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGC 466
Db        326 GTACCGCGTTGAGTTTTTCCACGTTAACGCTCACCGCAATTGCAATTGACAGATATATTC 385

Qy        467 ATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTC 526
Db        386 TCATCTGTCATCCGACGAAAGAACCGATACGCAAAGATCAAGCATTGAAAATGATAAGTT 445

Qy        527 TTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATG 570
Db        446 TCAACAGCGCCATCTCAGTTGGGCTTTCGGTACCATTATTCATG 489


RESULT 13
AR408548
LOCUS       AR408548               1352 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 15 from patent US 6632621.
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ACCESSION   AR408548
VERSION     AR408548.1  GI:40158788
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1352)
  AUTHORS   Lowery,D.E., Geary,T.G., Kubiak,T.M. and Larsen,M.J.
  TITLE     G protein-coupled receptor-like receptors and modulators thereof
  JOURNAL   Patent: US 6632621-A 15 14-OCT-2003;
            Pharmacia & Upjohn Company; Kalamazoo, MI
FEATURES             Location/Qualifiers
     source          1. .1352
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                     /mol_type="genomic DNA"
ORIGIN
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Query Match 6.6%; Score 78.8; DB 6; Length 1352;
Best Local Similarity 47.4%; Pred. No. 2.1e-11;
Matches 381; Conservative 0; Mismatches 402; Indels 21; Gaps 4;

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Qy        134 TCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCC 193
              || |||||   || ||   |||| |  | ||       |   || | || |||    ||
Db         56 TCAATGATTGGACAGTCCTCTTTGAAGTTCGGCTTGGATATTCAGTACTATACTTTCTCA 115

Qy        194 TGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAAACAAGC 253
              | ||  || | ||  |  |||||||| ||     |  |     |  |    |    |||
Db        116 TATTAATAATCGGATTGGTTGGAAATGGGCTATTGATCACTTCAATTTTAATGCGAAAGA 175

Qy        254 GGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATATTGG 313
                ||      |||    ||| ||||  || | ||| ||    |  | |||||| | |
Db        176 AACTTTCCGTGGC---AAACATATTCTTGATAAACCTGGCAGTTTCTGATTTGCTTCTTT 232

Qy        314 TGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGACTGGGCATTCGGGT 373
              ||||  |||  | ||  |||| |||    |  ||| | |  ||     |||  ||| ||
Db        233 GCATCACGGCGGTGCCGATCACTCCAGTATTGGCGTTTATGAAGCGATGGATATTTGGAA 292

Qy        374 CAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTTGTGACGAGTTGGA 433
              | | |||||  | || |||||     |   | ||| |||||||  |  |  |    |||
Db        293 TAATTATGTGTAAATTGGTTCCAACTTGTCAGGCGTTTTCGGTGCTCATTTCTTCATGGT 352

Qy        434 GCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCCACCAAACAACCAG 493
              |   |  ||| |  | |||| || ||    |||          ||   |    |||||
Db        353 CTTTGTGTTACATCGCAATTGATAGATATCGAAGTATTGTGACGCCACTCCGGGAACCAT 412

Qy        494 TTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTCTCAACACTGATAA 553
              |||  | | || ||   |    |    |  | |  ||| | ||| |    ||    |
Db        413 GGTCTGATAGGCATGCAAGGTGGCTTCTGATGTTCACATGGGTGGTCGCCTTCCTTGCTA 472

Qy        554 ATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTACGTTCAGCCCGGAG 613
              |    |||| | | | || |   ||  |    ||   |    || |      |
Db        473 GT------TATCCTCTATATTACTCACAGAACTTGAAAACAATGGTTATTGA------AA 520

Qy        614 AAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGCGAAAATAGTCGAA 673
              |    |||  || ||  | |||||||| ||||   |||||||||   ||  | |     |
Db        521 ATGTGACATTATGTGGAGATTTTTGCGGCGAGTTCAATTGGCAGTCGGATGAAATATCCA 580

Qy        674 AGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATGGCAGTGATCACGT 733
              || |       ||||||  | | ||| |       |  |       ||| | |||| ||
Db        581 AGTTGACATATACTACGAGTTTATTGATTATTCAGCTGATTATTCCAGCAATTATCATGT 640

Qy        734 ATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATCCAAAATGCTCAAT 793
              ||  |   |    |||  | | | ||  |  | ||  |      |     | |    ||
Db        641 CTTTTTGTTATTTAATGATTCTACAAAAGGTACAAACCGACTGGCTTGTCGACGAGGGAT 700

Qy        794 TCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGAAAGAAGAAAGTGA 853
              |      |     ||||| ||    ||  |  |        ||||||     |||||
Db        701 CCATGTTGACTGCCGCACAACAGGCTCAAACAGCAG------TTCGAAAGCGACGAGTGA 754

Qy        854 ATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTGCCTTTAACATTAC 913
              ||  |  | |||  ||||||| |    |||||  |  || |||||  || ||  |
Db        755 TGTACGTGTTGATTCTAATGGTTATTGTTTTTATGGCTTGCTGGTTCCCGTTGTCCGCCG 814
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Qy        914 TCAATTTGGTCAAAGATTTTAAAA 937
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Db        815 TGAATTTGTTCAGAGATCTCGGAA 838
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RESULT 14
AX151230
LOCUS       AX151230               1352 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 15 from Patent WO0138533.
ACCESSION   AX151230
VERSION     AX151230.1  GI:14533396
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lowery,D.E., Geary,T.G., Kubiak,T.M. and Larsen,M.J.
  TITLE     G protein-coupled receptor-like receptors and modulators thereof
  JOURNAL   Patent: WO 0138533-A 15 31-MAY-2001;
            PHARMACIA & UPJOHN COMPANY (US)
FEATURES             Location/Qualifiers
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                     /db_xref="GI:14533397"
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ORIGIN
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Query Match 6.6%; Score 78.8; DB 6; Length 1352;
Best Local Similarity 47.4%; Pred. No. 2.1e-11;
Matches 381; Conservative 0; Mismatches 402; Indels 21; Gaps 4;

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Qy        134 TCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCC 193
              || |||||   || ||   |||| |  | ||       |   || | || |||    ||
Db         56 TCAATGATTGGACAGTCCTCTTTGAAGTTCGGCTTGGATATTCAGTACTATACTTTCTCA 115

Qy        194 TGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAAACAAGC 253
              | ||  || | ||  |  |||||||| ||     |  |     |  |    |    |||
Db        116 TATTAATAATCGGATTGGTTGGAAATGGGCTATTGATCACTTCAATTTTAATGCGAAAGA 175

Qy        254 GGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATATTGG 313
                ||      |||    ||| ||||  || | ||| ||    |  | |||||| | |
Db        176 AACTTTCCGTGGC---AAACATATTCTTGATAAACCTGGCAGTTTCTGATTTGCTTCTTT 232

Qy        314 TGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGACTGGGCATTCGGGT 373
              ||||  |||  | ||  |||| |||    |  ||| | |  ||     |||  ||| ||
Db        233 GCATCACGGCGGTGCCGATCACTCCAGTATTGGCGTTTATGAAGCGATGGATATTTGGAA 292

Qy        374 CAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTTGTGACGAGTTGGA 433
              | | |||||  | || |||||     |   | ||| |||||||  |  |  |    |||
Db        293 TAATTATGTGTAAATTGGTTCCAACTTGTCAGGCGTTTTCGGTGCTCATTTCTTCATGGT 352

Qy        434 GCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCCACCAAACAACCAG 493
              |   |  ||| |  | |||| || ||    |||          ||   |    |||||
Db        353 CTTTGTGTTACATCGCAATTGATAGATATCGAAGTATTGTGACGCCACTCCGGGAACCAT 412

Qy        494 TTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTCTCAACACTGATAA 553
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Db        413 GGTCTGATAGGCATGCAAGGTGGCTTCTGATGTTCACATGGGTGGTCGCCTTCCTTGCTA 472

Qy        554 ATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTACGTTCAGCCCGGAG 613

Db        473 GT------TATCCTCTATATTACTCACAGAACTTGAAAACAATGGTTATTGA------AA 520

Qy        614 AAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGCGAAAATAGTCGAA 673

Db        521 ATGTGACATTATGTGGAGATTTTTGCGGCGAGTTCAATTGGCAGTCGGATGAAATATCCA 580

Qy        674 AGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATGGCAGTGATCACGT 733

Db        581 AGTTGACATATACTACGAGTTTATTGATTATTCAGCTGATTATTCCAGCAATTATCATGT 640

Qy        734 ATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATCCAAAATGCTCAAT 793

Db        641 CTTTTTGTTATTTAATGATTCTACAAAAGGTACAAACCGACTGGCTTGTCGACGAGGGAT 700

Qy        794 TCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGAAAGAAGAAAGTGA 853

Db        701 CCATGTTGACTGCCGCACAACAGGCTCAAACAGCAG------TTCGAAAGCGACGAGTGA 754

Qy        854 ATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTGCCTTTAACATTAC 913

Db        755 TGTACGTGTTGATTCTAATGGTTATTGTTTTTATGGCTTGCTGGTTCCCGTTGTCCGCCG 814

Qy        914 TCAATTTGGTCAAAGATTTTAAAA 937

Db        815 TGAATTTGTTCAGAGATCTCGGAA 838


RESULT 15
AF073925
LOCUS       AF073925               1315 bp    DNA     linear   VRT 10-AUG-2000
DEFINITION  Gadus morhua neuropeptide Y/peptide YY receptor Yb (NPYRb) gene,
            complete cds.
ACCESSION   AF073925
VERSION     AF073925.1  GI:4106396
KEYWORDS    .
SOURCE      Gadus morhua (Atlantic cod)
  ORGANISM  Gadus morhua
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
REFERENCE   1  (bases 1 to 1315)
  AUTHORS   Arvidsson,A.K., Wraith,A., Jonsson-Rylander,A.C. and Larhammar,D.
  TITLE     Cloning of a neuropeptide Y/peptide YY receptor from the Atlantic
            cod: the Yb receptor
  JOURNAL   Regul. Pept. 75-76, 39-43 (1998)
   PUBMED   9802392
REFERENCE   2  (bases 1 to 1315)
  AUTHORS   Arvidsson,A.-K., Wraith,A., Jonsson-Rylander,A.-C. and Larhammar,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUN-1998) Neuroscience, Uppsala University, Box 593,
            Uppsala SE-75123, Sweden
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             5.9%;  Score 69.8;  DB 5;  Length 1315;
  Best Local Similarity   45.0%;  Pred. No. 9.5e-09;
  Matches  263;  Conservative    0;  Mismatches  322;  Indels    0;  Gaps    0;

Qy        170 TCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTAC 229

Db        187 TCCTCATCCTGGTCTACAGCACCATGATCGCCGTGGGCATCGTGGGCAACTCTTGCCTGG 246

Qy        230 TATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACT 289

Db        247 TCTTCGTCATCGCCAGGCAGAAGGAGATGCACAACGTCACCAACATCTTCATCGCCAACC 306

Qy        290 TGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGA 349

Db        307 TGTCCTGCTCGGACATCCTCATGTGCATCTTCTGCCTGCCCGTCACGCTCATCTACACCC 366

Qy        350 TGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGT 409

Db        367 TGATGGACCGCTGGATCCTGGGGGAGGCCCTGTGCAAGCTCACCCCGTTCGTGCAGTGCA 426

Qy        410 GTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATA 469

Db        427 TCTCGGTGACGGTGTCCATCTTCTCCTTGGTTCTCATCGCCATGGAGCGCTACCAGCTCA 486

Qy        470 TCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTA 529

Db        487 TCATCCACCCCACGGGCTGGAAGCCCATGGTCGGCCAGTCCTACATGGCGGTGGGCATCA 546

Qy        530 TCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATG 589

Db        547 TCTGGGTGGTGGCCTGCCTCATCTCCGTGCCTTTCCTGTCCTTCACCGTGCTGGACAACC 606

Qy        590 GAAGCTTTTACGTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGA 649

Db        607 TGCCGCTCCAGAACCTCAGCCTCCCCTTCCCCGGCCAGGACCACTGGCTGTGCACAGAGA 666

Qy        650 ATTGGCAGAGCGAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCG 709

Db        667 GCTGGCCCACCAACAGCAACCGTCTGGCCTACACGACCTCCCTGCTGGTCTTCCAGTACT 726

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Job time : 6325 secs
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GenCore version 5.1.8

OM nucleic - nucleic search, using sw model

Run on: May 8, 2006, 14:28:24 ; Search time 5402 Seconds
(without alignments)
10332.653 Million cell updates/sec

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Perfect score: 1193
Sequence: 1 atggttagttcggcggccac.....tgtgcaggcaactctttcta 1193

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
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5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	684	57.3	801	7	CV124545	OSTF30030
2	579	48.5	615	3	BJ113336	BJ113336 BJ113336
3	509	42.7	543	3	BJ759866	BJ759866 BJ759866
c 4	471	39.5	749	3	BJ142720	BJ142720 BJ142720
5	435	36.5	469	3	BJ762291	BJ762291 BJ762291
6	360.4	30.2	366	3	BJ117135	BJ117135 BJ117135
c 7	297	24.9	713	3	BJ786750	BJ786750 BJ786750
8	257	21.5	258	3	BJ767176	BJ767176 BJ767176
9	153.4	12.9	530	3	BI451132	BI451132 kx11b03.y
c 10	102.4	8.6	477	3	BJ784215	BJ784215 BJ784215
c 11	100	8.4	445	3	BJ153679	BJ153679 BJ153679
c 12	85.6	7.2	608	10	CZ209081	CZ209081 AIAA-aad9
13	84	7.0	578	6	CB402398	CB402398 OSTF212A4
14	80	6.7	850	1	AI438264	AI438264 SWOvAFCAP
15	79.6	6.7	537	6	CB402411	CB402411 OSTF212C1
16	70.2	5.9	616	3	BJ763929	BJ763929 BJ763929
17	66.6	5.6	575	1	AU198665	AU198665 AU198665
18	66	5.5	794	8	CX796754	CX796754 JGI_CAAJ1
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20	64.8	5.4	813	5	BU363760	BU363760 603787987
21	64	5.4	661	3	BM278050	BM278050 As_tgz_52
22	62.8	5.3	820	6	CA939929	CA939929 ru75a09.y
23	62.6	5.2	709	1	AI943600	AI943600 BSBmMFSZ4
c 24	60.2	5.0	276	3	BJ144795	BJ144795 BJ144795
25	58.4	4.9	594	3	BP228990	BP228990 BP228990
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27	57.8	4.8	591	7	CV024564	CV024564 1977 Full
28	57.8	4.8	718	7	CO959636	CO959636 AGENCOURT
29	57.8	4.8	1152	10	AY413581	AY413581 Pan trogl
30	57.8	4.8	1155	10	AY413580	AY413580 Homo sapi
31	57.6	4.8	1168	10	AY409053	AY409053 Homo sapi
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33	56.8	4.8	803	6	CD559637	CD559637 AGENCOURT
34	56.6	4.7	515	2	BF286067	BF286067 EST450658
35	56.2	4.7	455	6	CB741495	CB741495 AMGNNUC:C
36	56	4.7	550	3	BJ108410	BJ108410 BJ108410
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39	55.2	4.6	706	8	DR982513	DR982513 JGI_AOKF5
40	55.2	4.6	718	8	DR985305	DR985305 JGI_AOKG5
c 41	55.2	4.6	718	8	DR985306	DR985306 JGI_AOKG5
c 42	55.2	4.6	728	8	DR982514	DR982514 JGI_AOKF5
c 43	55.2	4.6	737	8	DR983058	DR983058 JGI_AOKF8
44	55.2	4.6	795	6	CD559636	CD559636 AGENCOURT
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ALIGNMENTS

RESULT 1
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LOCUS CV124545 801 bp mRNA linear EST 31-AUG-2004
DEFINITION OSTF30030H01 pDONR201 Entry vector Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CV124545
VERSION CV124545.1 GI:51715739
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 801)
AUTHORS Lamesch,P., Milstein,S., Hao,T., Rosenberg,J., Li,N., Sequerra,R., Bosak,S., Doucette-Stamm,L., Vandenhaute,J., Hill,D.E. and Vidal,M.
TITLE C. elegans ORFeome Version 3.1: Increasing the coverage of ORFeome resources with improved gene predictions
JOURNAL Genome Res. (ORFeome issue) (2004) In press
COMMENT Contact: Philippe Lamesch and Tong Hao
Marc Vidal Lab
DFCI
44, Binney Street, Boston, MA 02115, USA
Tel: 6176323910
Fax: 6176325739
Email: philippe_lamesch@dfci.harvard.edu
PCR Primers
FORWARD: TGGTTAGTTCGGCGGCCACCATT
BACKWARD: TAGAAAGAGTTGCCTGCACAT.
FEATURES Location/Qualifiers
source 1. .801
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/db_xref="taxon:6239"
/sex="male and hermaphrodite"
/tissue_type="all tissues"
/cell_type="all cells"
/dev_stage="all stages"
/clone_lib="pDONR201 Entry vector"
ORIGIN

Query Match 57.3%; Score 684; DB 7; Length 801;
Best Local Similarity 98.3%; Pred. No. 1e-191;
Matches 702; Conservative 0; Mismatches 10; Indels 2; Gaps 1;

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Qy         62 GCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATTG 121
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Db         61 GCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATTG 120

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Db        121 CGGCACAAGGCATCGATGATATTACTGTAAACTTTTACATCCGATCAATCTTCACATTCC 180

Qy        182 TCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGG 241
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Db        181 TCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGG 240

Qy        242 CGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACCG 301
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Db        241 CGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACCG 300

Qy        302 ATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGACT 361
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Db        301 ATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGACT 360

Qy        362 GGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTTG 421
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Qy        422 TGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCCA 481
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Db        421 TGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCCA 480

Qy        482 CCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTCT 541
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Db        481 CCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTCT 540

Qy        542 CAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTACG 601
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Db        541 CAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTACG 600

Qy        602 TTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGCG 661
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LOCUS       BJ113336                615 bp    mRNA    linear   EST 23-JAN-2002
DEFINITION  BJ113336 unpublished oligo-capped cDNA library, C. elegans L1 stage
            Caenorhabditis elegans cDNA clone yk1166h04 5', mRNA sequence.
ACCESSION   BJ113336
VERSION     BJ113336.1  GI:18273407
KEYWORDS    EST.
SOURCE      Caenorhabditis elegans
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 615)
  AUTHORS   Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
            and Sugano,S.
  TITLE     A complementary view of the C.elegans genome
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
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                     /clone="yk1166h04"
                     /sex="hermaphrodite"
                     /tissue_type="whole animal"
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                     /clone_lib="unpublished oligo-capped cDNA library, C.
                     elegans L1 stage"
ORIGIN
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Qy          1 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 60
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Db         36 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 95

Qy         61 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120
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Db         96 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 155

Qy        121 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 180
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Db        156 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 215

Qy        181 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 240
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Db        216 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 275

Qy        241 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 300
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Db        276 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 335

Qy        301 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 360
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Qy        361 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 420
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Db        516 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 575

Qy        541 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGC 580
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RESULT 3
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DEFINITION  BJ759866 unpublished oligo-capped cDNA library Caenorhabditis
            elegans cDNA clone yk1532c11 5', mRNA sequence.
ACCESSION   BJ759866
VERSION     BJ759866.1  GI:47599628
KEYWORDS    EST.
SOURCE      Caenorhabditis elegans
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 543)
  AUTHORS   Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
```

and Sugano,S.
TITLE A complementary view of the C.elegans genome
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES Location/Qualifiers
source 1. .543
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/clone="yk1532c11"
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/clone_lib="unpublished oligo-capped cDNA library"
ORIGIN

Query Match 42.7%; Score 509; DB 3; Length 543;
Best Local Similarity 100.0%; Pred. No. 1.1e-139;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120
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Qy        181 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 240
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Qy        301 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 360
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Qy        481 ACCAAACAACCAGTTTCTATTCGTCAAGC 509
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Db        515 ACCAAACAACCAGTTTCTATTCGTCAAGC 543
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RESULT 4
BJ142720/c
LOCUS BJ142720 749 bp mRNA linear EST 23-JAN-2002
DEFINITION BJ142720 unpublished oligo-capped cDNA library, C. elegans L1 stage Caenorhabditis elegans cDNA clone yk1187g06 3', mRNA sequence.
ACCESSION BJ142720
VERSION BJ142720.1 GI:18302886
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 749)
AUTHORS Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y. and Sugano,S.
TITLE A complementary view of the C.elegans genome
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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/clone="yk1187g06"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"
/clone_lib="unpublished oligo-capped cDNA library, C. elegans L1 stage"
ORIGIN

Query Match 39.5%; Score 471; DB 3; Length 749;
Best Local Similarity 100.0%; Pred. No. 2.5e-128;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        723 AGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATCCA 782
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Db        749 AGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATCCA 690

Qy        783 AAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGAAA 842
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        689 AAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGAAA 630

Qy        843 GAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTGCC 902
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        629 GAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTGCC 570

Qy        903 TTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGTCA 962
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        569 TTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGTCA 510

Qy        963 GCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAACCC 1022
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        509 GCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAACCC 450

Qy       1023 TCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTCAA 1082
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        449 TCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTCAA 390

Qy       1083 CTCAACAGAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAGGGATCCAGCTACACGA 1142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 CTCAACAGAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAGGGATCCAGCTACACGA 330

Qy       1143 CCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 1193
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Db        329 CCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 279
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RESULT 5
BJ762291
LOCUS BJ762291 469 bp mRNA linear EST 25-MAY-2004
DEFINITION BJ762291 unpublished oligo-capped cDNA library Caenorhabditis elegans cDNA clone yk1585h05 5', mRNA sequence.
ACCESSION BJ762291
VERSION BJ762291.1 GI:47621159

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KEYWORDS    EST.
SOURCE      Caenorhabditis elegans
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 469)
  AUTHORS   Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
            and Sugano,S.
  TITLE     A complementary view of the C.elegans genome
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .469
                     /organism="Caenorhabditis elegans"
                     /mol_type="mRNA"
                     /strain="N2"
                     /db_xref="taxon:6239"
                     /clone="yk1585h05"
                     /sex="Hermaphrodite"
                     /tissue_type="whole animal"
                     /dev_stage="varied"
                     /clone_lib="unpublished oligo-capped cDNA library"
ORIGIN

  Query Match             36.5%;  Score 435;  DB 3;  Length 469;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-117;
  Matches  435;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         35 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 94

Qy         61 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         95 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 154

Qy        121 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 180
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Db        155 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 214

Qy        181 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 240
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Db        215 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 274

Qy        241 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 300
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Db        275 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 334

Qy        301 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        335 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 394

Qy        361 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 454

Qy        421 GTGACGAGTTGGAGC 435
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Db        455 GTGACGAGTTGGAGC 469


RESULT 6
BJ117135
LOCUS       BJ117135                366 bp    mRNA    linear   EST 23-JAN-2002
DEFINITION  BJ117135 unpublished oligo-capped cDNA library, C. elegans L1 stage
            Caenorhabditis elegans cDNA clone yk1211c12 5', mRNA sequence.
ACCESSION   BJ117135
VERSION     BJ117135.1  GI:18277247
KEYWORDS    EST.
SOURCE      Caenorhabditis elegans
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 366)
  AUTHORS   Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
            and Sugano,S.
  TITLE     A complementary view of the C.elegans genome
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .366
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                     /mol_type="mRNA"
                     /strain="N2"
                     /db_xref="taxon:6239"
                     /clone="yk1211c12"
                     /sex="hermaphrodite"
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                     /dev_stage="L1"
                     /clone_lib="unpublished oligo-capped cDNA library, C.
                     elegans L1 stage"
ORIGIN

  Query Match             30.2%;  Score 360.4;  DB 3;  Length 366;
  Best Local Similarity   98.6%;  Pred. No. 1.7e-95;
  Matches  361;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         40 ACAACGACTCCCTCCACCATCAGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGC 99
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db          1 ACAACGACTCCCTCCACCATCANCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGC 60

Qy        100 ATTCAGATCGCTGAGGCGATTGCGGCACAAGGCATCGATGATATTACTGTAGACTTTTAC 159
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db         61 ATTCAGATCGCTGAGGCGATTGCGGCACAAGGCATCGATGATGTTACTGTAGACTTTTAC 120

Qy        160 ATCCGATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAAC 219
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Db        121 ATCCGATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAAC 180

Qy        220 GGCGGCGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTT 279
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        181 GGCGGCGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGNTCGCAACGTATTN 240

Qy        280 CTGCTCAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCA 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGCTCAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCA 300

Qy        340 TGGTACGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTG 399
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        301 TGGTACGCGATGACCAAAGACTGGGCATTCGGGTCANTGATGTGCCATTTAGTTCCTTTG 360

Qy        400 TCAAAT 405
              ||||||
Db        361 TCAAAT 366


RESULT 7
BJ786750/c
LOCUS       BJ786750                713 bp    mRNA    linear   EST 25-MAY-2004
DEFINITION  BJ786750 unpublished oligo-capped cDNA library Caenorhabditis
            elegans cDNA clone yk1585h05 3', mRNA sequence.
ACCESSION   BJ786750
VERSION     BJ786750.1  GI:47665547
KEYWORDS    EST.
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SOURCE      Caenorhabditis elegans
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 713)
  AUTHORS   Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
            and Sugano,S.
  TITLE     A complementary view of the C.elegans genome
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /strain="N2"
                     /db_xref="taxon:6239"
                     /clone="yk1585h05"
                     /sex="Hermaphrodite"
                     /tissue_type="whole animal"
                     /dev_stage="varied"
                     /clone_lib="unpublished oligo-capped cDNA library"
ORIGIN

  Query Match             24.9%;  Score 297;  DB 3;  Length 713;
  Best Local Similarity   83.7%;  Pred. No. 1.5e-76;
  Matches  381;  Conservative    0;  Mismatches    0;  Indels   74;  Gaps    1;

Qy        813 AAAGCAGAGAAGTGATGCGACGTCACGAAAGAAGAAAGTGAATTATATTCTAATTGCAAT 872
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Db        713 AAAGCAGAGAAGTGATGCGACGTCACGAAAGAAGAAAGTGAATTATATTCTAATTGCAAT 654

Qy        873 GGTTGTCACATTTATCGGGTGTTGGTTGCCTTTAACATTACTCAATTTGGTCAAAGATTT 932
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Db        653 GGTTGTCACATTTATCGGGTGTTGGTTGCCTTTAACATTACTCAATTTGGTCAAAGATTT 594

Qy        933 TAAAAAAGAGCCCGAATGGCTAAAACGTCAGCCGTTCTTCTGGGCAATAAATGCTCACGT 992
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 TAAAAAAGAGCCCGAATGGCTAAAACGTCAGCCGTTCTTCTGGGCAATAAATGCTCACGT 534

Qy        993 CATAGCCATGTCCTTAGTCGTCTGGAACCCTCTGCTATTCTTTTGGCTGACACGAAAACA 1052
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 CATAGCCATGTCCTTAGTCGTCTGGAACCCTCTGCTATTCTTTTGGCTGACACGAAAACA 474

Qy       1053 AAAACGTTCCGGACTGTCAAAAATACTCAACTCAACAG---------------------- 1090
              ||||||||||||||||||||||||||||||||||||
Db        473 AAAACGTTCCGGACTGTCAAAAATACTCAACTCAACAGAGATTGTGTCCTCGTTTGCCAG 414

Qy       1091 ----------------------------------------------------AGGGTTCG 1098
                                                                    ||||||||
Db        413 TAGAGTGAGTAACTCGATTCGGCGGTCAACGTTTCGGAGAAACAATATTGACAGGGTTCG 354

Qy       1099 AAAAAAGCAGGTGGTTCTGGATTGCGAGGGATCCAGCTACACGACCTCCTCCCGACCTCT 1158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 AAAAAAGCAGGTGGTTCTGGATTGCGAGGGATCCAGCTACACGACCTCCTCCCGACCTCT 294

Qy       1159 ACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 1193
              ||||||||||||||||||||||||||||||||||
Db        293 ACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 259


RESULT 8
BJ767176
LOCUS       BJ767176                258 bp    mRNA    linear   EST 25-MAY-2004
DEFINITION  BJ767176 unpublished oligo-capped cDNA library Caenorhabditis
            elegans cDNA clone yk1655f07 5', mRNA sequence.
ACCESSION   BJ767176
VERSION     BJ767176.1  GI:47630881
KEYWORDS    EST.
SOURCE      Caenorhabditis elegans
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 258)
  AUTHORS   Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
            and Sugano,S.
  TITLE     A complementary view of the C.elegans genome
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /strain="N2"
                     /db_xref="taxon:6239"
                     /clone="yk1655f07"
                     /sex="Hermaphrodite"
                     /tissue_type="whole animal"
                     /dev_stage="varied"
                     /clone_lib="unpublished oligo-capped cDNA library"
ORIGIN

  Query Match             21.5%;  Score 257;  DB 3;  Length 258;
  Best Local Similarity   99.6%;  Pred. No. 8.8e-65;
  Matches  257;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         64 AACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATTGCG 123
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATTGCG 60

Qy        124 GCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTC 183
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTC 120

Qy        184 TACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGGCG 243
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGGCG 180

Qy        244 AGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACCGAT 303
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACCGAT 240

Qy        304 TTGATATTGGTGTTCACA 321
              |||||||||| |||||||
Db        241 TTGATATTGGNGTTCACA 258


RESULT 9
BI451132
LOCUS       BI451132                530 bp    mRNA    linear   EST 21-AUG-2001
DEFINITION  kx11b03.y3 Parastrongyloides trichosuri IL pAMP1 v1 Chiapelli
            McCarter Parastrongyloides trichosuri cDNA 5' similar to WP:CE24480
            Y58G8A.3 seven trans-membrane receptor ;, mRNA sequence.
ACCESSION   BI451132
VERSION     BI451132.1  GI:15275839
KEYWORDS    EST.
SOURCE      Parastrongyloides trichosuri
  ORGANISM  Parastrongyloides trichosuri
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Panagrolaimoidea; Strongyloididae; Parastrongyloides.
REFERENCE   1  (bases 1 to 530)
  AUTHORS   McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
            Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
            Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
            Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
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            Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
            Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
            McCann,R., Waterston,R. and Wilson,R.
  TITLE     The Washington Univ. Nematode EST Project, 1999
  JOURNAL   Unpublished (1999)
COMMENT     Contact: McCarter JP
            The Washington Univ. Nematode EST Project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            The library was constructed by Brandi Chiapelli and Dr. James
            McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu) at
            Washington University, St. Louis. DNA Sequencing by: Washington
            University Genome Sequencing Center St. Louis.
            High quality sequence stop: 384.
FEATURES             Location/Qualifiers
     source          1. .530
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                     /db_xref="taxon:131310"
                     /dev_stage="Infective Larvae"
                     /lab_host="DH10B"
                     /clone_lib="Parastrongyloides trichosuri IL pAMP1 v1
                     Chiapelli McCarter"
                     /note="Vector: pAMP1 (Gibco); Site_1: NotI; Site_2: SalI;
                     The library was constructed by Brandi Chiapelli and Dr.
                     James  McCarter at Washington University, St. Louis. The
                     cDNA was  made by using Dynabead oligo-dT priming (Dynal).
                     PCR based  library using a modified protocol from the
                     SMART PCR cDNA Synthesis  Kit from Clontech. Directionally
                     cloned into the UDG sites of pAMP1.  Nematodes were
                     provided by Dr. Warwick Grant of AgRearch, New Zealand
                     (warwick.grant@agresearch.co.nz)."
ORIGIN

  Query Match             12.9%;  Score 153.4;  DB 3;  Length 530;
  Best Local Similarity   57.5%;  Pred. No. 7.3e-34;
  Matches  296;  Conservative    0;  Mismatches  216;  Indels    3;  Gaps    1;

Qy        409 TGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCAT 468
              ||| | || ||||| |  ||||||     |    |||||| |  ||||||||||| | |||
Db         11 TGTGCCGTTTTTGTTAGCAGTTGGTCTTTATGTGCAATAGCACTAGATAAATTTATTCAT 70

Qy        469 ATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTT 528
              ||     |||| |  |  |||||||| || ||   ||||||       ||||||| |||||
Db         71 ATTGTAAATCCTATTAGGCAACCAGTATCAATAAATCAAGCAACTATAATAACAATTCTT 130

Qy        529 ATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGAT 588
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Db        131 ATATGGATATTATCAATTCTAGCAAATATTCCACCTATTGTTAATTCTGATCTCAAATCG 190

Qy        589 GGA---AGCTTTTACGTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAG 645
              |||     ||||      |      | |||  |     |   |     |||      ||
Db        191 GGAGATGCCTTTACAAGTTCATTTGAAGATAAAAAACCATTATGTGGAGTTTTTTGTGAA 250

Qy        646 GCGAATTGGCAGAGCGAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAG 705
              | ||  ||| | |      |   || | |  || |||   |  |    |  | || ||
Db        251 GAGACATGGGAAAATATGTCGACGAGACAAACGTATGGATTAATTGCATTAATTTTCCAA 310

Qy        706 TTCGTCGTGCCGATGGCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCA 765
              ||  | || ||  |||| | | || || |||||  |||| | |||  | || |||||  |
Db        311 TTTATTGTACCAATGGGAATAATAACATATTGTTACTGGAGAATTCTTCATAAAGTTGCT 370

Qy        766 AAAGACATGATCATCCAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGT 825
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Db        371 AAAGATTCAATAATTCACAATGTTCAATTTTCAAATTCATTATCAGCATCACAACGAAAT 430

Qy        826 GATGCGACGTCACGAAAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTT 885
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Db        431 GCTGCTATCAATAGAAAGAGACGAGTAAATTATATTTTAATTGCCATGGTATTAGCTTTT 490

Qy        886 ATCGGGTGTTGGTTGCCTTTAACATTACTCAATTT 920
              ||    |||||||| || ||||||  |    ||| |
Db        491 ATATTATGTTGGTTTCCGTTAACAATTTATAATAT 525


RESULT 10
BJ784215/c
LOCUS       BJ784215                477 bp    mRNA    linear   EST 25-MAY-2004
DEFINITION  BJ784215 unpublished oligo-capped cDNA library Caenorhabditis
            elegans cDNA clone yk1532c11 3', mRNA sequence.
ACCESSION   BJ784215
VERSION     BJ784215.1  GI:47663012
KEYWORDS    EST.
SOURCE      Caenorhabditis elegans
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 477)
  AUTHORS   Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
            and Sugano,S.
  TITLE     A complementary view of the C.elegans genome
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
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                     /strain="N2"
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                     /clone="yk1532c11"
                     /sex="Hermaphrodite"
                     /tissue_type="whole animal"
                     /dev_stage="varied"
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ORIGIN

  Query Match              8.6%;  Score 102.4;  DB 3;  Length 477;
  Best Local Similarity   98.1%;  Pred. No. 1.1e-18;
  Matches  103;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1089 AGAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAGGGATCCAGCTACACGACCTCCT 1148
              | |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        359 ACAGGGTTCGAAAAAAGCAGGTGGTTNTGGATTGCGAGGGATCCAGCTACACGACCTCCT 300

Qy       1149 CCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 1193
              |||||||||||||||||||||||||||||||||||||||||||||
Db        299 CCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 255


RESULT 11
BJ153679/c
LOCUS       BJ153679                445 bp    mRNA    linear   EST 24-JAN-2002
DEFINITION  BJ153679 unpublished oligo-capped cDNA library, C. elegans L1 stage
            Caenorhabditis elegans cDNA clone yk1322b09 3', mRNA sequence.
ACCESSION   BJ153679
VERSION     BJ153679.1  GI:18321664
KEYWORDS    EST.
SOURCE      Caenorhabditis elegans
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 445)
  AUTHORS   Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
            and Sugano,S.
  TITLE     A complementary view of the C.elegans genome
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
```

```
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES              Location/Qualifiers
     source           1. .445
                      /organism="Caenorhabditis elegans"
                      /mol_type="mRNA"
                      /strain="N2"
                      /db_xref="taxon:6239"
                      /clone="yk1322b09"
                      /sex="hermaphrodite"
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                      /dev_stage="L1"
                      /clone_lib="unpublished oligo-capped cDNA library, C.
                      elegans L1 stage"
ORIGIN

  Query Match             8.4%;  Score 100;  DB 3;  Length 445;
  Best Local Similarity   97.1%;  Pred. No. 5.4e-18;
  Matches  100;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1091 AGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAGGGATCCAGCTACACGACCTCCTCC 1150
             ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        373 AGGGTTCGAAAAAAGCAGGTGGTTNTGGATTGCGAGGGATCCAGCTACACGACCTCCTCC 314

Qy       1151 CGACCTCTACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 1193
             |||||| |||||||||||||||||||||||||||||| ||
Db        313 CGACCTNTACTCATTCGGACAGATGTGCAGGCAACTCTTTNTA 271


RESULT 12
CZ209081/c
LOCUS       CZ209081                608 bp    DNA     linear   GSS 10-FEB-2005
DEFINITION  AIAA-aad99i10.g1 Ancylostoma caninum whole genome shotgun library
            (AIAAGSS 001) Ancylostoma caninum genomic, genomic survey sequence.
ACCESSION   CZ209081
VERSION     CZ209081.1  GI:59212954
KEYWORDS    GSS.
SOURCE      Ancylostoma caninum (dog hookworm)
  ORGANISM  Ancylostoma caninum
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
            Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
REFERENCE   1  (bases 1 to 608)
  AUTHORS   Mitreva,M., McCarter,J.P., Pape,D., Ritter,E., Tsagareishvili,R.,
            Ronko,I., Martin,J., Wylie,T., Dante,M., Meyer,R., Messina,D.,
            Waterston,R.H., Clifton,S.W. and Wilson,R.
  TITLE     Genome Survey sequences from the parasitic nematode Ancylostoma
            caninum
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Mitreva M
            Washington University in St. Louis
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: nematode@watson.wustl.edu
            Genomic DNA provided by John Hawdon (mtmjmh@gwumc.edu) DNA
            sequenced by Washington University Genome Sequencing Center
            Class: shotgun.
FEATURES              Location/Qualifiers
     source           1. .608
                      /organism="Ancylostoma caninum"
                      /mol_type="genomic DNA"
                      /strain="Baltimore"
                      /db_xref="taxon:29170"
                      /dev_stage="Adult"
                      /lab_host="GS10"
                      /clone_lib="Ancylostoma caninum whole genome shotgun
                      library (AIAAGSS 001)"
                      /note="Vector: pOTW13; Site_1: BstX1; Site_2: BstX1;
                      Ancylostoma caninum genomic DNA was randomly sheared,
                      end-repaired and size fractioned to enrich for 2-4 kb
                      fragments. Genomic DNA was provided by John Hawdon
                      (mtmjmh@gwumc.edu) at George Washington University.
                      Sequencing by Washington University Genome Sequencing
                      Center, St. Louis, MO."
ORIGIN

  Query Match             7.2%;  Score 85.6;  DB 10;  Length 608;
  Best Local Similarity   64.8%;  Pred. No. 1.1e-13;
  Matches  127;  Conservative    0;  Mismatches   69;  Indels    0;  Gaps    0;

Qy        152 ACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTT 211
              | || | | ||  |||    |||||  || |||||||| || |||||  || | ||  |
Db        319 AATTGTTCGTCAAATCGGCGTTCACGCTCGTCTACGGCTTTCTGTTCATACTTGGTCTCG 260

Qy        212 TTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCA 271
              | || || || |||||  |||  ||  ||||||  ||    || || |  || ||  | |
Db        259 TCGGCAATGGTGGCGTCGTATTTGCAATGGCGAATAATCGCCGACTACGGTCAGCCAGGA 200

Qy        272 ACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAG 331
              || |||| |||||||| ||||  |||| ||| || || | ||  |||| ||  | || |
Db        199 ACATATTCCTGCTCAATCTGATACTCACTGATCTGCTACTTGTACTCACTGCCGTACCTG 140

Qy        332 TCACACCATGGTACGC 347
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Db        139 TTACGCCTTGGTAGGC 124


RESULT 13
CB402398
LOCUS       CB402398                578 bp    mRNA    linear   EST 15-MAY-2003
DEFINITION  OSTF212A4_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION   CB402398
VERSION     CB402398.1  GI:30744125
KEYWORDS    EST.
SOURCE      Caenorhabditis elegans
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 578)
  AUTHORS   Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
            Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,
            Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
            Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,
            Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
            Doucette-Stamm,L., Hill,D.E. and Vidal,M.
  TITLE     C. elegans ORFeome version 1.1: experimental verification of the
            genome annotation and resource for proteome-scale protein
            expression
  JOURNAL   Nat. Genet. (2003) In press
COMMENT     Contact: Vidal M
            Marc Vidal Laboratory
            Dana Farber Cancer Institute
            1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
            Tel: 617 632 5180
            Fax: 617 632 5739
            Email: Marc_Vidal@dfci.harvard.edu
            Sequence tag of Gateway entry clones. The primers used were
            designed on the predicted protein encoding ORF. C. elegans ORFeome
            cloning project : Contact david_hill@dfci.harvard.edu or
            marc_vidal@dfci.harvard.edu
            POLYA=No.
FEATURES              Location/Qualifiers
     source           1. .578
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                      /mol_type="mRNA"
                      /strain="N2"
                      /db_xref="taxon:6239"
                      /sex="Hermaphrodite and male"
                      /tissue_type="whole animal"
                      /dev_stage="mixed stage"
                      /clone_lib="AD-wrmcDNA"
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/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

ORIGIN

Query Match 7.0%; Score 84; DB 6; Length 578;
Best Local Similarity 50.5%; Pred. No. 3.3e-13;
Matches 204; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

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Qy        167 CAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCG 226
              | ||  |  ||  | |||||   |  |  | ||| | ||| |     || ||       |
Db         85 CGATTCTTGCAACCATCTACACTATAATTGTCGTAGTTGGCGTAACCGGCAATTTGTTAG 144

Qy        227 TACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCA 286
              ||  |  | |||||  |||   |||    || |||||  |   | ||| | ||  |  |
Db        145 TAGTGATGTCGGTGATGAGGTTCAAAGTTCTTCAATCAGTCAGGAACATGTTCATCGTAT 204

Qy        287 ACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACG 346
              |||     |  | ||  |  | ||| | |          | |||| || ||       ||
Db        205 CTTTGTCAGTTTCTGACATTTTTGTGGCGATTGTTAGTGGTTCAGTAACGCCGATAACCG 264

Qy        347 CGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATT 406
              |  |  |||| |||  ||| ||  |    |||| |||||| | ||||||| | |
Db        265 CATTCTCTAAAGTTTGGTTATTTGGTGGACCATTGTGTCATTTACTACCTTTGTTACAGG 324

Qy        407 CGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGC 466
                || ||  | |  | |  |  | ||||| |||||  |  | || | || | | |
Db        325 GTACCGCGTTGAGTTTTTCCACGTTAACGCTCACCGCAATTGCAATTGACAGATATATTC 384

Qy        467 ATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTC 526
              |||    |||| || ||| |||  |    |    |||||| ||| ||| | |  |
Db        385 TCATCTGTCATCCGACGAAAGAACCGATACGCAAAGATCAAGCATTGAAAATGATAAGTT 444

Qy        527 TTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATG 570
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Db        445 TCAACAGCGCCATCTCAGTTGGGCTTTCGGTACCATTATTCATG 488
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RESULT 14
AI438264
LOCUS AI438264 850 bp mRNA linear EST 09-MAR-1999
DEFINITION SWOvAFCAP29C10SK Onchocerca volvulus adult female cDNA (SAW98MLW-OvAF) Onchocerca volvulus cDNA clone SWOvAFCAP29C10 5', mRNA sequence.
ACCESSION AI438264
VERSION AI438264.1 GI:4294956
KEYWORDS EST.
SOURCE Onchocerca volvulus
ORGANISM Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerca.
REFERENCE 1 (bases 1 to 850)
AUTHORS Lizotte-Waniewski,M. and Williams,S.A.
TITLE Genes expressed in adult female stage of Onchocerca volvulus
JOURNAL Unpublished (1998)
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
FEATURES Location/Qualifiers
source 1. .850
/organism="Onchocerca volvulus"
/mol_type="mRNA"
/db_xref="taxon:6282"
/clone="SWOvAFCAP29C10"
/sex="female"
/dev_stage="adult"
/lab_host="XL1-Blue MRF'"
/clone_lib="Onchocerca volvulus adult female cDNA (SAW98MLW-OvAF)"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Two adult female worms of Onchocerca volvulus were isolated from consenting patients and quick frozen. Adult female mRNA was converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 7 x 10E5 independent recombinants and the average insert size is ~1100bp.The library was constructed by Michelle Lizotte-Waniewski with worms provided by Dr. Sara Lustigman. The library is available from Dr.Steven A. Williams, email: genome@smith.edu."

ORIGIN

Query Match 6.7%; Score 80; DB 1; Length 850;
Best Local Similarity 50.2%; Pred. No. 5.8e-12;
Matches 205; Conservative 0; Mismatches 202; Indels 1; Gaps 1;

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              |||  | |    |  |  | |  ||  ||||||   ||  | |||||     |  |
Db        167 GATTGGAGTACTCAGTCATCTACCGTATTCATCTTCGTTTTTTTTTACGGAGCANTTATC 226

Qy        199 GTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAAACAAGCGGCTC 258
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Db        227 CTGATCGGTNTAGTGGGCAACCTGTGCGTCATACTGGCCATATCTAGGACCAGGACACTG 286

Qy        259 CAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATATTGGTGTTC 318
              ||| |    | |||  | ||  |  |    |||| ||   ||||  |  |  |    ||
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Qy        319 ACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGACTGGGCATTCGGGTCAGTG 378
              ||  |   || | ||  ||     ||  | |  ||||| |||    |||||  | ||
Db        347 ACTTCAGCGACAATNACGCCGNTCACGGCNTTCAAAAAAGAGTGGATCTTCGGTGCTGTA 406

Qy        379 ATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTTGTGACGAGTTGGAGCCTC 438
              | |||     ||| ||| ||       |    |||  |||    |  | |  |   |||
Db        407 CTCTGCTCGATAGCTCCGTTTATTGCTGGCACTTCACTGTGCTTCTCCACGTTTACTCTC 466

Qy        439 ACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCCACCAAACAACCAGTTTCT 498
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Db        467 TCAGCANTCTCAGTGGATCGTTTTTTGCTCATCTATTTTCCGACTAGAAAAGCTCTTTCC 526

Qy        499 ATTCGTC-AAGCGTTGGCAATAACATTTCTTATCTGGATAGTCTCAAC 545
              |  | || |||| ||     |||   |  |  | || ||| | || ||
Db        527 AGGCTTCAAAGCATTNNTCGTAATTATGGTNNTNTGCATATTATCCAC 574
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RESULT 15
CB402411
LOCUS CB402411 537 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTF212C1_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB402411
VERSION CB402411.1 GI:30744138
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 537)
AUTHORS Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S., Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H., Doucette-Stamm,L., Hill,D.E. and Vidal,M.
TITLE C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression
JOURNAL Nat. Genet. (2003) In press
COMMENT Contact: Vidal M

Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc_Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu
POLYA=No.

FEATURES Location/Qualifiers
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/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

ORIGIN

Query Match 6.7%; Score 79.6; DB 6; Length 537;
Best Local Similarity 50.0%; Pred. No. 6.7e-12;
Matches 199; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

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              || ||| |  |   |   |  |||||    | | | ||  |||| ||||||  | |  |
Db         32 GAAGATTTGTCATCAAGGTGGTACATAATGTTAGTGTTTGCATTTCTCTACCTGATAATC 91

Qy        196 TTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAAACAAGCGG 255
               |||     || ||  ||||||||    | ||  | | |||  |  | || |||||
Db         92 ATTGCCGCCGGAATAATTGGAAACTCATGTGTGATTTTGGCAATCACAAGGAACAAATCA 151

Qy        256 CTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATATTGGTG 315
              || ||| | | ||  ||  | ||| | ||    ||    |   | ||| |  |  |
Db        152 CTTCAAACTGTTCCGAATCTGTTTATTCTTTCTTTATCATGTTCTGATATTGTGGTATGC 211

Qy        316 TTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGACTGGGCATTCGGGTCA 375
              | |||| |     || |||| ||        ||  | |  ||||| |||   || ||
Db        212 TGCACATCTGCAACAATCACTCCGATTACTGCATTCAAGAAAGAATGGATCTTTGGAGAG 271

Qy        376 GTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTTGTGACGAGTTGGAGC 435
              |   | ||||   | |  || ||      |          | | | |  | | ||  |
Db        272 GCTTTATGCCGAATTGCACCATTCATTGCTGGTATCAGCCTTTGTTTCTCAACTTTCACA 331

Qy        436 CTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCCACCAAACAACCAGTT 495
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Db        332 TTGACTGCAATCTCCATCGACAGATACATCCTGATTCGATTTCCGATGAGGAAACCTATT 391

Qy        496 TCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTG 533
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Db        392 ACGCATTATCAAGCGGTTGGAGTGATTGCTATTATTTG 429
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GenCore version 5.1.8

OM nucleic - nucleic search, using sw model

Run on: May 8, 2006, 14:20:34 ; Search time 811 Seconds
(without alignments)
9803.919 Million cell updates/sec

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Perfect score: 1193
Sequence: 1 atggttagttcggcggccac.....tgtgcaggcaactctttcta 1193

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: geneseqn2002as:*
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10: geneseqn2003cs:*
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13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1193	100.0	1193	4	AAS07253	Aas07253 G protein
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3	1109	93.0	1301	4	AAS07254	Aas07254 G protein
4	96.6	8.1	1130	4	AAS07210	Aas07210 G protein
5	84	7.0	1098	4	AAS07217	Aas07217 G protein
6	78.8	6.6	1352	4	AAS07208	Aas07208 G protein
7	66.6	5.6	1374	4	AAS07212	Aas07212 G protein
8	62.2	5.2	1965	2	AAQ25892	Aaq25892 Sequence
9	62.2	5.2	2018	10	ADB52872	Adb52872 Primary r
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11	61.6	5.2	1302	12	ADL32476	Adl32476 Human neu
12	61.6	5.2	1302	14	ADW80001	Adw80001 Human neu
13	61.6	5.2	1302	14	ADZ76145	Adz76145 Human neu
14	61.6	5.2	1440	3	AAA57839	Aaa57839 DNA encod
15	61.6	5.2	1560	10	ACH00816	Ach00816 Human neu
16	61.6	5.2	1560	14	ADZ14210	Adz14210 Human neu
17	61.6	5.2	1569	12	ADO29937	Ado29937 Human GPC
18	61.6	5.2	1569	14	ADV43737	Adv43737 Human psy
19	61.6	5.2	1790	5	AAS00315	Aas00315 Orphan re
20	61.6	5.2	1824	4	ABA08967	Aba08967 Human GPC
21	61.6	5.2	1888	2	AAV68484	Aav68484 Human 7-t
22	61.6	5.2	1888	3	AAA61230	Aaa61230 DNA encod
23	61.6	5.2	1888	6	ABK47410	Abk47410 Human cDN
24	61.6	5.2	1903	3	AAZ86955	Aaz86955 Human NPY
25	61.6	5.2	1903	14	ADY84708	Ady84708 Human neu
26	61.6	5.2	1936	8	ABZ42862	Abz42862 Human neu
27	61.6	5.2	1936	10	ADC89683	Adc89683 Human neu
28	61.6	5.2	1936	10	ADE85182	Ade85182 Farnesyl
29	61.6	5.2	1936	12	ADH61950	Adh61950 Human neu
30	61.6	5.2	1936	12	ADQ21327	Adq21327 Human sof
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32	61.6	5.2	1938	12	ADQ25198	Adq25198 Human sof
33	60.2	5.0	1557	5	AAH49408	Aah49408 D. melano
34	60.2	5.0	1803	5	AAS05844	Aas05844 Fruit fly
35	60.2	5.0	1803	9	AAD57459	Aad57459 Fruit fly
36	60.2	5.0	1803	10	ADE14523	Ade14523 DNA encod
37	60.2	5.0	1803	11	ADL83601	Adl83601 Drosophil
38	60.2	5.0	1803	12	ADR03091	Adr03091 Drosophil
39	60.2	5.0	1803	14	ADV91971	Adv91971 DmGPCR1 c
40	60.2	5.0	2504	4	ABL29487	Abl29487 Drosophil
41	60.2	5.0	16870	4	ABL29486	Abl29486 Drosophil
42	60	5.0	1934	5	AAS00316	Aas00316 Orphan re
43	58.4	4.9	2708	2	AAV69220	Aav69220 Human G-p
44	57.8	4.8	1155	10	AAD62456	Aad62456 Human neu
45	57.8	4.8	1155	10	ADH53331	Adh53331 Human neu

ALIGNMENTS

RESULT 1
AAS07253
ID AAS07253 standard; DNA; 1193 BP.
XX
AC AAS07253;
XX
DT 12-SEP-2001 (first entry)
XX
DE G protein-coupled receptor-like (GPCR-like) receptor DNA #23.
XX
KW G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;
KW endoparasite; ectoparasite; invertebrate; insect; neurological disorder;
KW neuromuscular disorder; human; nematode; ds.
XX
OS Homo sapiens.
XX
PN WO200138533-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-US032225.
XX
PR 24-NOV-1999; 99US-0167523P.
XX
PA (PHAA) PHARMACIA & UPJOHN.
XX
PI Lowery DE, Geary TG, Kubiak TM, Larsen MJ;
XX
DR WPI; 2001-343952/36.
DR P-PSDB; AAU03851.
XX
PT Using G-protein-coupled receptor (GPCR)-like receptors to identify
PT candidate compounds for the treatment and prevention of invertebrate
PT parasites, especially helminths and insects.
XX
PS Claim 1; Page 173-175; 219pp; English.
XX
CC The sequence represents a DNA encoding a G protein-coupled receptor-like
CC (GPCR-like) receptor protein. GPCR-like receptors and their associated
CC nucleic acids may be used to identify candidate compounds for their
CC ability to modulate the activity of GPCRs. The sequences therefore are
CC useful for treating and preventing infection by endoparasitic and

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CC   ectoparasitic invertebrate parasites, especially helminths and insects,
CC   and particularly ailments related to aberrant neurological and
CC   neuromuscular function
XX
SQ   Sequence 1193 BP; 326 A; 281 C; 256 G; 330 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 1193;  DB 4;  Length 1193;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1193;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 60

Qy         61 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120

Qy        121 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 180

Qy        181 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 240

Qy        241 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 300

Qy        301 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 360

Qy        361 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 420

Qy        421 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC 480

Qy        481 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 540

Qy        541 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC 600

Qy        601 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 660

Qy        661 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 720

Qy        721 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 780

Qy        781 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 840

Qy        841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900

Qy        901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960

Qy        961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020

Qy       1021 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1080

Qy       1081 AACTCAACAGAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAGGGATCCAGCTACAC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AACTCAACAGAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAGGGATCCAGCTACAC 1140

Qy       1141 GACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 1193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 1193


RESULT 2
AAS07219
ID   AAS07219 standard; DNA; 1500 BP.
XX
AC   AAS07219;
XX
DT   12-SEP-2001  (first entry)
XX
DE   G protein-coupled receptor-like (GPCR-like) receptor DNA #19.
XX
KW   G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;
KW   endoparasite; ectoparasite; invertebrate; insect; neurological disorder;
KW   neuromuscular disorder; human; nematode; ds.
XX
OS   Homo sapiens.
XX
PN   WO200138533-A2.
XX
PD   31-MAY-2001.
XX
PF   24-NOV-2000; 2000WO-US032225.
XX
PR   24-NOV-1999;   99US-0167523P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN.
XX
PI   Lowery DE,  Geary TG,  Kubiak TM,  Larsen MJ;
XX
DR   WPI; 2001-343952/36.
DR   P-PSDB; AAU03820.
XX
PT   Using G-protein-coupled receptor (GPCR)-like receptors to identify
PT   candidate compounds for the treatment and prevention of invertebrate
PT   parasites, especially helminths and insects.
XX
PS   Claim 1; Page 145-147; 219pp; English.
XX
CC   The sequence represents a DNA encoding a G protein-coupled receptor-like
CC   (GPCR-like) receptor protein. GPCR-like receptors and their associated
CC   nucleic acids may be used to identify candidate compounds for their
CC   ability to modulate the activity of GPCRs. The sequences therefore are
CC   useful for treating and preventing infection by endoparasitic and
CC   ectoparasitic invertebrate parasites, especially helminths and insects,
CC   and particularly ailments related to aberrant neurological and
CC   neuromuscular function
XX
SQ   Sequence 1500 BP; 426 A; 322 C; 291 G; 461 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 1193;  DB 4;  Length 1500;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1193;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 366
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Qy        61 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       367 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 426

Qy       121 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       427 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 486

Qy       181 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       487 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 546

Qy       241 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       547 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 606

Qy       301 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       607 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 666

Qy       361 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       667 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 726

Qy       421 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       727 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC 786

Qy       481 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       787 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 846

Qy       541 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       847 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC 906

Qy       601 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       907 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 966

Qy       661 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       967 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 1026

Qy       721 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1027 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 1086

Qy       781 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1087 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 1146

Qy       841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1147 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 1206

Qy       901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1207 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 1266

Qy       961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1267 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1326

Qy      1021 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1327 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1386

Qy      1081 AACTCAACAGAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAGGGATCCAGCTACAC 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1387 AACTCAACAGAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAGGGATCCAGCTACAC 1446

Qy      1141 GACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 1193
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1447 GACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 1499
```

RESULT 3
AAS07254
ID AAS07254 standard; DNA; 1301 BP.
XX
AC AAS07254;
XX
DT 12-SEP-2001 (first entry)
XX
DE G protein-coupled receptor-like (GPCR-like) receptor DNA #24.
XX
KW G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;
KW endoparasite; ectoparasite; invertebrate; insect; neurological disorder;
KW neuromuscular disorder; human; nematode; ds.
XX
OS Homo sapiens.
XX
PN WO200138533-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-US032225.
XX
PR 24-NOV-1999; 99US-0167523P.
XX
PA (PHAA) PHARMACIA & UPJOHN.
XX
PI Lowery DE, Geary TG, Kubiak TM, Larsen MJ;
XX
DR WPI; 2001-343952/36.
DR P-PSDB; AAU03852.
XX
PT Using G-protein-coupled receptor (GPCR)-like receptors to identify
PT candidate compounds for the treatment and prevention of invertebrate
PT parasites, especially helminths and insects.
XX
PS Claim 1; Page 177-178; 219pp; English.
XX
CC The sequence represents a DNA encoding a G protein-coupled receptor-like
CC (GPCR-like) receptor protein. GPCR-like receptors and their associated
CC nucleic acids may be used to identify candidate compounds for their
CC ability to modulate the activity of GPCRs. The sequences therefore are
CC useful for treating and preventing infection by endoparasitic and
CC ectoparasitic invertebrate parasites, especially helminths and insects,
CC and particularly ailments related to aberrant neurological and
CC neuromuscular function
XX
SQ Sequence 1301 BP; 353 A; 304 C; 286 G; 358 T; 0 U; 0 Other;

Query Match 93.0%; Score 1109; DB 4; Length 1301;
Best Local Similarity 94.2%; Pred. No. 0;
Matches 1193; Conservative 0; Mismatches 0; Indels 74; Gaps 1;

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Qy          1 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 60

Qy         61 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120

Qy        121 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 180

Qy        181 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 240
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Qy       241 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 300
Db       241 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 300

Qy       301 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 360
Db       301 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 360

Qy       361 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 420
Db       361 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 420

Qy       421 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC 480
Db       421 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC 480

Qy       481 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 540
Db       481 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 540

Qy       541 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC 600
Db       541 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC 600

Qy       601 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 660
Db       601 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 660

Qy       661 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 720
Db       661 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 720

Qy       721 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 780
Db       721 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 780

Qy       781 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 840
Db       781 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 840

Qy       841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900
Db       841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900

Qy       901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960
Db       901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960

Qy       961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020
Db       961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020

Qy      1021 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1080
Db      1021 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1080

Qy      1081 AACTCAACAG---------------------------------------------------- 1090
Db      1081 AACTCAACAGAGATTGTGTCCTCGTTTGCCAGTAGAGTGAGTAACTCGATTCGGCGGTCA 1140

Qy      1091 ------------------------AGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAG 1126
Db      1141 ACGTTTCGGAGAAACAATATTGACAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAG 1200

Qy      1127 GGATCCAGCTACACGACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACT 1186
Db      1201 GGATCCAGCTACACGACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACT 1260

Qy      1187 CTTTCTA 1193
Db      1261 CTTTCTA 1267
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RESULT 4
AAS07210
ID   AAS07210 standard; DNA; 1130 BP.
XX
AC   AAS07210;
XX
DT   12-SEP-2001  (first entry)
XX
DE   G protein-coupled receptor-like (GPCR-like) receptor DNA #10.
XX
KW   G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;
KW   endoparasite; ectoparasite; invertebrate; insect; neurological disorder;
KW   neuromuscular disorder; human; nematode; ds.
XX
OS   Homo sapiens.
XX
PN   WO200138533-A2.
XX
PD   31-MAY-2001.
XX
PF   24-NOV-2000; 2000WO-US032225.
XX
PR   24-NOV-1999;   99US-0167523P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN.
XX
PI   Lowery DE,  Geary TG,  Kubiak TM,  Larsen MJ;
XX
DR   WPI; 2001-343952/36.
DR   P-PSDB; AAU03811.
XX
PT   Using G-protein-coupled receptor (GPCR)-like receptors to identify
PT   candidate compounds for the treatment and prevention of invertebrate
PT   parasites, especially helminths and insects.
XX
PS   Claim 1; Page 116-118; 219pp; English.
XX
CC   The sequence represents a DNA encoding a G protein-coupled receptor-like
CC   (GPCR-like) receptor protein. GPCR-like receptors and their associated
CC   nucleic acids may be used to identify candidate compounds for their
CC   ability to modulate the activity of GPCRs. The sequences therefore are
CC   useful for treating and preventing infection by endoparasitic and
CC   ectoparasitic invertebrate parasites, especially helminths and insects,
CC   and particularly ailments related to aberrant neurological and
CC   neuromuscular function
XX
SQ   Sequence 1130 BP; 340 A; 241 C; 225 G; 324 T; 0 U; 0 Other;

  Query Match             8.1%;  Score 96.6;  DB 4;  Length 1130;
  Best Local Similarity   47.0%;  Pred. No. 1.1e-18;
  Matches  438;  Conservative    0;  Mismatches  454;  Indels   39;  Gaps    3;

Qy       136 GATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCCTG 195
Db        52 GAAGATTTGTCATCAAGGTGGTACATAATGTTAGTGTTTGCATTTCTCTACCTGATAATC 111

Qy       196 TTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAAACAAGCGG 255
Db       112 ATTGCCGCCGGAATAATTGGAAACTCATGTGTGATTTTGGCAATCACAAGGAACAAATCA 171

Qy       256 CTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATATTGGTG 315
Db       172 CTTCAAACTGTTCCGAATCTGTTTATTCTTTCTTTATCATGTTCTGATATTGTGGTATGC 231

Qy       316 TTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGACTGGGCATTCGGGTCA 375
Db       232 TGCACATCTGCAACAATCACTCCGATTACTGCATTCAAGAAAGAATGGATCTTTGGAGAG 291

Qy       376 GTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTTGTGACGAGTTGGAGC 435
Db       292 GCTTTATGCCGAATTGCACCATTCATTGCTGGTATCAGCCTTTGTTTCTCAACTTTCACA 351

Qy       436 CTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCCACCAAACAACCAGTT 495
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Db        352 TTGACTGCAATCTCCATCGACAGATACATCCTGATTCGATTTCCGATGAGGAAACCTATT 411

Qy        496 TCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTCTCAACACTGATAAAT 555

Db        412 ACGCATTATCAAGCGGTTGGAGTGATTGCTATTATTTGCGCTTTTGCTGCAACCATCA-- 469

Qy        556 CTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTACGTTCAGCCCGGAGAA 615

Db        470 ----CATCCCCAATAATGTTCAAGCAAAAGCTGGGAGAGTTTGAGAAT------------ 513

Qy        616 ACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGCGAAAATAGTCGAAAG 675

Db        514 ------TTTTGTGGGCAGTACTGCACGGAAAACTGGGGAGCCAATGAAAGCCAGAGAAAA 567

Qy        676 ATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATGGCAGTGATCACGTAT 735

Db        568 ATTTATGGTGCAGCTCTGATGTTTCTTCAGCTCGTCATTCCGCTTACCATCATCATCATA 627

Qy        736 TGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATCCAAAATGCTCAATTC 795

Db        628 TCCTACACTGCGATTTCTTTGAAGATCGGACAAAGCATGATTCTCAAAGGGGCGAAAAAG 687

Qy        796 TGTCAATCACTGA---------------CACAAAAGCAGAGAAGTGATGCGACGTCACGA 840

Db        688 CAAAAAACAGACAATTGGGAAATGGAATTAAGTGATCAACAAAGAATCGCTGTGAAGAGA 747

Qy        841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900

Db        748 AGACAAAGAACTAATAGAATGCTTATTGGTATGGTAGTCGCATTCGCTTGCAGCTGGATT 807

Qy        901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960

Db        808 TGGTCAGTGACGTTCAACATTCTGAGGGACTATGAATATTTGCCAGAGCTCATCAAAACT 867

Qy        961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020

Db        868 CAAGAATATATCTTTGGAATTGCTACACATTGCATTGCAATGACCTCAACGGTATGGAAC 927

Qy       1021 CCTCTGCTATTCTTTTGGCTGACACGAAAAC 1051

Db        928 CCGTTACTCTACGCAGTGCTCAACCTCCAAC 958
```

```
RESULT 5
AAS07217
ID   AAS07217 standard; DNA; 1098 BP.
XX
AC   AAS07217;
XX
DT   12-SEP-2001  (first entry)
XX
DE   G protein-coupled receptor-like (GPCR-like) receptor DNA #17.
XX
KW   G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;
KW   endoparasite; ectoparasite; invertebrate; insect; neurological disorder;
KW   neuromuscular disorder; human; nematode; ds.
XX
OS   Homo sapiens.
XX
PN   WO200138533-A2.
XX
PD   31-MAY-2001.
XX
PF   24-NOV-2000; 2000WO-US032225.
XX
PR   24-NOV-1999;   99US-0167523P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN.
XX
PI   Lowery DE,  Geary TG,  Kubiak TM,  Larsen MJ;
XX
DR   WPI; 2001-343952/36.
DR   P-PSDB; AAU03818.
XX
PT   Using G-protein-coupled receptor (GPCR)-like receptors to identify
PT   candidate compounds for the treatment and prevention of invertebrate
PT   parasites, especially helminths and insects.
XX
PS   Claim 1; Page 139-141; 219pp; English.
XX
CC   The sequence represents a DNA encoding a G protein-coupled receptor-like
CC   (GPCR-like) receptor protein. GPCR-like receptors and their associated
CC   nucleic acids may be used to identify candidate compounds for their
CC   ability to modulate the activity of GPCRs. The sequences therefore are
CC   useful for treating and preventing infection by endoparasitic and
CC   ectoparasitic invertebrate parasites, especially helminths and insects,
CC   and particularly ailments related to aberrant neurological and
CC   neuromuscular function
XX
SQ   Sequence 1098 BP; 280 A; 250 C; 230 G; 338 T; 0 U; 0 Other;

  Query Match             7.0%;  Score 84;  DB 4;  Length 1098;
  Best Local Similarity   50.5%;  Pred. No. 8.7e-15;
  Matches  204;  Conservative    0;  Mismatches  200;  Indels    0;  Gaps    0;

Qy        167 CAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCG 226

Db         86 CGATTCTTGCAACCATCTACACTATAATTGTCGTAGTTGGCGTAACCGGCAATTTGTTAG 145

Qy        227 TACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCA 286

Db        146 TAGTGATGTCGGTGATGAGGTTCAAAGTTCTTCAATCAGTCAGGAACATGTTCATCGTAT 205

Qy        287 ACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACG 346

Db        206 CTTTGTCAGTTTCTGACATTTTTGTGGCGATTGTTAGTGGTTCAGTAACGCCGATAACCG 265

Qy        347 CGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATT 406

Db        266 CATTCTCTAAAGTTTGGTTATTTGGTGGACCATTGTGTCATTTACTACCTTTGTTACAGG 325

Qy        407 CGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGC 466

Db        326 GTACCGCGTTGAGTTTTTCCACGTTAACGCTCACCGCAATTGCAATTGACAGATATATTC 385

Qy        467 ATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTC 526

Db        386 TCATCTGTCATCCGACGAAAGAACCGATACGCAAAGATCAAGCATTGAAAATGATAAGTT 445

Qy        527 TTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATG 570

Db        446 TCAACAGCGCCATCTCAGTTGGGCTTTCGGTACCATTATTCATG 489
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```
RESULT 6
AAS07208
ID   AAS07208 standard; DNA; 1352 BP.
XX
AC   AAS07208;
XX
DT   12-SEP-2001  (first entry)
XX
DE   G protein-coupled receptor-like (GPCR-like) receptor DNA #8.
XX
KW   G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;
KW   endoparasite; ectoparasite; invertebrate; insect; neurological disorder;
KW   neuromuscular disorder; human; nematode; ds.
XX
OS   Homo sapiens.
XX
PN   WO200138533-A2.
XX
PD   31-MAY-2001.
XX
PF   24-NOV-2000; 2000WO-US032225.
```

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XX
PR   24-NOV-1999;   99US-0167523P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN.
XX
PI   Lowery DE,  Geary TG,  Kubiak TM,  Larsen MJ;
XX
DR   WPI; 2001-343952/36.
DR   P-PSDB; AAU03809.
XX
PT   Using G-protein-coupled receptor (GPCR)-like receptors to identify
PT   candidate compounds for the treatment and prevention of invertebrate
PT   parasites, especially helminths and insects.
XX
PS   Claim 1; Page 108-110; 219pp; English.
XX
CC   The sequence represents a DNA encoding a G protein-coupled receptor-like
CC   (GPCR-like) receptor protein. GPCR-like receptors and their associated
CC   nucleic acids may be used to identify candidate compounds for their
CC   ability to modulate the activity of GPCRs. The sequences therefore are
CC   useful for treating and preventing infection by endoparasitic and
CC   ectoparasitic invertebrate parasites, especially helminths and insects,
CC   and particularly ailments related to aberrant neurological and
CC   neuromuscular function
XX
SQ   Sequence 1352 BP; 337 A; 284 C; 307 G; 424 T; 0 U; 0 Other;

  Query Match             6.6%;  Score 78.8;  DB 4;  Length 1352;
  Best Local Similarity   47.4%;  Pred. No. 3.9e-13;
  Matches  381;  Conservative    0;  Mismatches  402;  Indels   21;  Gaps    4;

Qy        134 TCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCC 193
              || ||||||   || ||   |||| |  | ||        |   || | || |||    ||
Db         56 TCAATGATTGGACAGTCCTCTTTGAAGTTCGGCTTGGATATTCAGTACTATACTTTCTCA 115

Qy        194 TGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAAACAAGC 253
              | ||  || | ||  |  ||||||| ||      |  |      |  |     |    |||
Db        116 TATTAATAATCGGATTGGTTGGAAATGGGCTATTGATCACTTCAATTTTAATGCGAAAGA 175

Qy        254 GGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATATTGG 313
                ||      |||    ||| ||||  || | ||| ||    |  | |||||| |  |
Db        176 AACTTTCCGTGGC---AAACATATTCTTGATAAACCTGGCAGTTTCTGATTTGCTTCTTT 232

Qy        314 TGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGACTGGGCATTCGGGT 373
              ||||  ||| | ||  |||| |||   |  ||| | |  ||    |||  ||| ||
Db        233 GCATCACGGCGGTGCCGATCACTCCAGTATTGGCGTTTATGAAGCGATGGATATTTGGAA 292

Qy        374 CAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTTGTGACGAGTTGGA 433
              | | |||||  | || |||||     |   |  ||| |||||||  |  |  |    |||
Db        293 TAATTATGTGTAAATTGGTTCCAACTTGTCAGGCGTTTTCGGTGCTCATTTCTTCATGGT 352

Qy        434 GCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCCACCAAACAACCAG 493
                |   |  ||| |  | |||| || ||    |||         ||    |    |||||
Db        353 CTTTGTGTTACATCGCAATTGATAGATATCGAAGTATTGTGACGCCACTCCGGGAACCAT 412

Qy        494 TTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTCTCAACACTGATAA 553
              |||  | | ||  ||    |     |  | |  |||  | |||  |     ||    |
Db        413 GGTCTGATAGGCATGCAAGGTGGCTTCTGATGTTCACATGGGTGGTCGCCTTCCTTGCTA 472

Qy        554 ATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTACGTTCAGCCCGGAG 613
                |      |||| | | | ||  |    ||   |      ||    |    || |      |
Db        473 GT------TATCCTCTATATTACTCACAGAACTTGAAAACAATGGTTATTGA------AA 520

Qy        614 AAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGCGAAAATAGTCGAA 673
              |     |||  || ||  | |||||||| ||||   |||||||||   ||  | |     |
Db        521 ATGTGACATTATGTGGAGATTTTTGCGGCGAGTTCAATTGGCAGTCGGATGAAATATCCA 580

Qy        674 AGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATGGCAGTGATCACGT 733
              || |       ||||||  | | ||| |       |   |       ||| | |||| ||
Db        581 AGTTGACATATACTACGAGTTTATTGATTATTCAGCTGATTATTCCAGCAATTATCATGT 640

Qy        734 ATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATCCAAAATGCTCAAT 793
                ||  |  |   |||  | | | ||  |  | ||  |       |     | |   ||
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Db        641 CTTTTTGTTATTTAATGATTCTACAAAAGGTACAAACCGACTGGCTTGTCGACGAGGGAT 700

Qy        794 TCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGAAAGAAGAAAGTGA 853
                |      |     ||||| ||     ||  |  |       ||||||     |||||
Db        701 CCATGTTGACTGCCGCACAACAGGCTCAAACAGCAG------TTCGAAAGCGACGAGTGA 754

Qy        854 ATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTGCCTTTAACATTAC 913
                ||  |  | |||  |||||||  |     |||||  |  || |||||  || ||  |
Db        755 TGTACGTGTTGATTCTAATGGTTATTGTTTTTATGGCTTGCTGGTTCCCGTTGTCCGCCG 814

Qy        914 TCAATTTGGTCAAAGATTTTAAAA 937
              | ||||||  ||| ||||  |   ||
Db        815 TGAATTTGTTCAGAGATCTCGGAA 838


RESULT 7
AAS07212
ID   AAS07212 standard; DNA; 1374 BP.
XX
AC   AAS07212;
XX
DT   12-SEP-2001  (first entry)
XX
DE   G protein-coupled receptor-like (GPCR-like) receptor DNA #12.
XX
KW   G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;
KW   endoparasite; ectoparasite; invertebrate; insect; neurological disorder;
KW   neuromuscular disorder; human; nematode; ds.
XX
OS   Homo sapiens.
XX
PN   WO200138533-A2.
XX
PD   31-MAY-2001.
XX
PF   24-NOV-2000; 2000WO-US032225.
XX
PR   24-NOV-1999;   99US-0167523P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN.
XX
PI   Lowery DE,  Geary TG,  Kubiak TM,  Larsen MJ;
XX
DR   WPI; 2001-343952/36.
DR   P-PSDB; AAU03813.
XX
PT   Using G-protein-coupled receptor (GPCR)-like receptors to identify
PT   candidate compounds for the treatment and prevention of invertebrate
PT   parasites, especially helminths and insects.
XX
PS   Claim 1; Page 122-124; 219pp; English.
XX
CC   The sequence represents a DNA encoding a G protein-coupled receptor-like
CC   (GPCR-like) receptor protein. GPCR-like receptors and their associated
CC   nucleic acids may be used to identify candidate compounds for their
CC   ability to modulate the activity of GPCRs. The sequences therefore are
CC   useful for treating and preventing infection by endoparasitic and
CC   ectoparasitic invertebrate parasites, especially helminths and insects,
CC   and particularly ailments related to aberrant neurological and
CC   neuromuscular function
XX
SQ   Sequence 1374 BP; 402 A; 280 C; 296 G; 396 T; 0 U; 0 Other;

  Query Match             5.6%;  Score 66.6;  DB 4;  Length 1374;
  Best Local Similarity   48.3%;  Pred. No. 2.3e-09;
  Matches  186;  Conservative    0;  Mismatches  199;  Indels    0;  Gaps    0;

Qy        180 CCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGT 239
              | | |||   || || ||| |  | ||  | |||||||| |    | |  | |  |
Db         93 CGTGTACCTTTTTCTCTTTTTTCTTGGACTCTTTGGAAATGTGACCTTGATTTACGTAAC 152

Qy        240 GGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCAC 299
                  ||  | ||     | |     | ||  ||| ||||  | || ||| ||      |
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Db        153 TTGCAGCCATAAAGCTTTACTGAGCGTTCAAAACATATTCATTCTGAACCTGGCGGCGAG 212

Qy        300 CGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGA 359

Db        213 CGATTGCATGATGTGCATATTATCGCTTCCAATCACTCCAATCACAAATGTGTACAAAAA 272

Qy        360 CTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTT 419

Db        273 CTGGTACTTTGGAAATCTACTCTGCCATTTGATACCATGCATTCAAGGTATCAGCATTTT 332

Qy        420 TGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCC 479

Db        333 CGTATGCACATTCAGTCTCGGTGCGATTGCTTTGGATCGGTATATCCTTGTAGTAAGACC 392

Qy        480 CACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGT 539

Db        393 ACATTCTACACCACTATCCCAAAGAGGAGCATTTCTTACTACTGTTCTATTGTGGATCCT 452

Qy        540 CTCAACACTGATAAATCTACCGTAT 564

Db        453 CTCTTTTGTTGTAACTCTACCCTAT 477
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RESULT 8
AAQ25892
ID   AAQ25892 standard; cDNA; 1965 BP.
XX
AC   AAQ25892;
XX
DT   25-MAR-2003  (revised)
DT   23-SEP-1992  (first entry)
XX
DE   Sequence encodes endothelin receptor.
XX
KW   endothelin; vasoconstrictor peptide; endothelial cells; hypertension;
KW   sarafotoxin.
XX
OS   Rattus rattus.
XX
FH   Key             Location/Qualifiers
FT   3'UTR           1. .201
FT                   /*tag=  b
FT                   /label
FT                   /note= "3'UTR in mRNA of the endothelin receptor encoded
FT                   by this mRNA contains AUUUA sequence which destabilises
FT                   mRNA. This is analogous to transiently expressed cytokine
FT                   or GF."
FT   CDS             202. .1524
FT                   /*tag=  a
FT                   /product= "endothelin_receptor"
XX
PN   EP480381-A.
XX
PD   15-APR-1992.
XX
PF   08-OCT-1990;   90JP-00270172.
XX
PR   08-OCT-1990;   90JP-00270172.
XX
PA   (NICM ) NIPPON CHEMIPHAR CO.
XX
PI   Sakurai T,  Yanigasawa M,  Masaki T;
XX
DR   WPI; 1992-125055/16.
DR   P-PSDB; AAR25394.
XX
PT   DNA encoding endothelin receptors - new agents contg. the receptor are
PT   useful in diagnosing hypertension or hypotension.
XX
PS   Disclosure; 13; 27pp; English.
XX
CC   This sequence was deduced as follows. A cDNA library was prepared by
CC   reverse transcription of polyA RNA isolated from rat lung. This was
CC   screened by direct expression of mRNA from DNA fragments accumulated in
CC   monkey COS-7 cells using mammalian expression vector pCDM8, which
CC   contains a replicating initiation point of SV40 and polyoma,and another
CC   replication initiation point of cytomegalovirus/T7RNA polymerase
CC   prom,oter and M13. The cells expressing biologically active endothelin
CC   receptor were identified by incubating transfected COS-7 cells in a
CC   culture containing [125I- Tyr13] endothelin-1, and detecting with X-ray
CC   film. Positive cells were then rescreened, a clone isolated and its
CC   sequence of insertion fragments analysed to determine the cDNA sequence
CC   of rat endothelin receptor. See also AAR25394. (Updated on 25-MAR-2003 to
CC   correct PR field.)
XX
SQ   Sequence 1965 BP; 529 A; 467 C; 467 G; 502 T; 0 U; 0 Other;

  Query Match             5.2%;  Score 62.2;  DB 2;  Length 1965;
  Best Local Similarity   50.5%;  Pred. No. 6.4e-08;
  Matches  151;  Conservative    0;  Mismatches  148;  Indels    0;  Gaps    0;

Qy        165 ATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGG 224

Db        501 ATACATCAACACGATTGTATCATGCCTCGTGTTCGTGCTAGGCATCATCGGGAACTCCAC 560

Qy        225 CGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT 284

Db        561 ACTGCTAAGAATCATCTACAAGAACAAGTGCATGAGAAATGGTCCCAATATCTTGATCGC 620

Qy        285 CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTA 344

Db        621 CAGCCTGGCTCTGGGAGATCTGCTACACATCATCATCGACATTCCCATTAATGCCTACAA 680

Qy        345 CGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAA 404

Db        681 GCTGCTGGCAGGGGACTGGCCATTTGGAGCTGAGATGTGCAAGCTGGTGCCCTTCATACA 740

Qy        405 TTCGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTC 463

Db        741 GAAGGCTTCTGTGGGGATCACAGTGTTGAGTCTATGTGCTCTAAGTATTGACAGATATC 799
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RESULT 9
ADB52872
ID   ADB52872 standard; DNA; 2018 BP.
XX
AC   ADB52872;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3414.
XX
KW   toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
KW   toxicity marker; toxicity progression; drug screening;
KW   primary rat hepatocyte toxicity modelling; gene; ds.
XX
OS   Rattus norvegicus.
XX
PN   WO2003065993-A2.
XX
PD   14-AUG-2003.
XX
PF   04-FEB-2003; 2003WO-US003482.
XX
PR   04-FEB-2002; 2002US-0353171P.
PR   13-MAR-2002; 2002US-0363534P.
PR   08-APR-2002; 2002US-0370248P.
PR   10-APR-2002; 2002US-0371134P.
PR   10-APR-2002; 2002US-0371135P.
PR   10-APR-2002; 2002US-0371150P.
PR   11-APR-2002; 2002US-0371413P.
PR   19-APR-2002; 2002US-0373601P.
PR   19-APR-2002; 2002US-0373602P.
PR   22-APR-2002; 2002US-0374139P.
PR   08-MAY-2002; 2002US-0378370P.
PR   09-MAY-2002; 2002US-0378652P.
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PR 09-MAY-2002; 2002US-0378653P.
PR 09-MAY-2002; 2002US-0378665P.
PR 09-JUL-2002; 2002US-0394230P.
PR 09-JUL-2002; 2002US-0394253P.
PR 04-SEP-2002; 2002US-0407688P.
PR 28-JAN-2003; 2003US-0442900P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;
PI Elashoff M;
XX
DR WPI; 2003-731472/69.
XX
PT Determining if a compound induces a toxic effect on a tissue or cell, for
PT identifying hepatotoxic compounds, comprises comparing a gene expression
PT profile of a tissue or cell sample to a database of Tox mean and non-Tox
PT mean values.
XX
PS Claim 44; SEQ ID NO 3414; 874pp; English.
XX
CC The present invention describes a method for determining whether a
CC compound induces a toxic effect on a tissue or cell. The method comprises
CC preparing a gene expression profile of a tissue or cell sample exposed to
CC the compound, and comparing the gene expression profile to a database
CC comprising data or information on the Tox mean and non-Tox mean value.
CC The method is useful for predicting or identifying at least one toxic
CC effect, particularly hepatotoxicity, of a test or unknown compound. The
CC genes listed in the specification are useful as diagnostic or toxicity
CC markers for the prediction or identification of the physiological state
CC of tissue or cell sample that has been exposed to a compound, or to
CC identify or predict the toxic effects of a compound or an agent. These
CC may also be used as markers for monitoring toxicity progression or for
CC drug screening. The present sequence represents a primary rat hepatocyte
CC toxicity modelling related gene sequence from the present invention.
XX
SQ Sequence 2018 BP; 540 A; 491 C; 485 G; 502 T; 0 U; 0 Other;

Query Match 5.2%; Score 62.2; DB 10; Length 2018;
Best Local Similarity 50.5%; Pred. No. 6.5e-08;
Matches 151; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

Qy 165 ATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGG 224
Db 554 ATACATCAACACGATTGTATCATGCCTCGTGTTCGTGCTAGGCATCATCGGGAACTCCAC 613

Qy 225 CGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT 284
Db 614 ACTGCTAAGAATCATCTACAAGAACAAGTGCATGAGAAATGGTCCCAATATCTTGATCGC 673

Qy 285 CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTA 344
Db 674 CAGCCTGGCTCTGGGAGATCTGCTACACATCATCATCGACATTCCCATTAATGCCTACAA 733

Qy 345 CGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAA 404
Db 734 GCTGCTGGCAGGGGACTGGCCATTTGGAGCTGAGATGTGCAAGCTGGTGCCCTTCATACA 793

Qy 405 TTCGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTC 463
Db 794 GAAGGCTTCTGTGGGGATCACAGTGTTGAGTCTATGTGCTCTAAGTATTGACAGATATC 852

RESULT 10
AAZ94667
ID AAZ94667 standard; cDNA; 1302 BP.
XX
AC AAZ94667;
XX
DT 01-AUG-2000 (first entry)
XX
DE Human neuropeptide FF (NPFF2) receptor cDNA.
XX
KW Neuropeptide FF receptor; NPFF2 receptor; human; antiinflammatory;
KW antiasthmatic; antidiabetic; immunostimulant; immunosuppressive;
KW nootropic; neuroprotective; analgesic; anoretic; antipsychotic;
KW antiaddictive; antimigraine; hypertensive; hypotensive; cardiant;
KW antiasthmatic; gene therapy; plasmid cDNA3.1-hNPFF2b;
KW G protein coupled receptor; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 31. .1293
FT /*tag= a
XX
PN WO200018438-A1.
XX
PD 06-APR-2000.
XX
PF 24-SEP-1999; 99WO-US022384.
XX
PR 25-SEP-1998; 98US-00161113.
PR 22-FEB-1999; 99US-00255368.
XX
PA (SYNA-) SYNAPTIC PHARM CORP.
XX
PI Gerald CPG, Jones KA, Bonini JA, Borowsky B;
XX
DR WPI; 2000-293017/25.
DR P-PSDB; AAY79375.
XX
PT Nucleic acid encoding a mammalian neuropeptide FF (NPFF) receptor, useful
PT for treatment of e.g pain, obesity, diabetes, hypertension, hypotension,
PT hypoglycemia, respiratory disorders.
XX
PS Claim 24; Fig 7; 253pp; English.
XX
CC The present sequence is that of human neuropeptide FF (NPFF2) receptor
CC cDNA, isolated from spleen cDNA by 5'/3'RACE. The cDNA contained in
CC plasmid pcDNA3.1-hNPFF2b is deposited as ATCC 203255. Highest levels of
CC NPFF2 RNA are found in the placenta, indicating a role in gestational
CC regulation. NPFF2 is also expressed in the central nervous system and
CC peripheral tissue. It may be involved in modulation of learning and
CC memory and in the regulation of fear, pain and analgesia, and may provide
CC a target for treatment of depression, anxiety, phobias and mood
CC disorders. Localisation to the caudate/putamen implies regulation of
CC dopaminergic systems and a role in the regulation of extrapyramidal motor
CC systems. The invention provides rat and human NPFF polypeptides and
CC polynucleotides, vectors, host cells, antibodies, nucleic acid probes,
CC antisense oligonucleotides, transgenic animals, methods of isolating
CC mammalian NPFF receptors, methods of treating an abnormality associated
CC with NPFF receptor activity, methods of determining binding of compounds
CC to NPFF receptors, methods of identifying agonists and antagonists of
CC NPFF receptors, and the agonists and antagonists obtained. Claimed
CC methods of treating an abnormality that is alleviated by
CC increasing/decreasing NPFF activity involve administering an NPFF
CC receptor agonist/antagonist. The abnormality is a lower urinary tract
CC disorder, an epinephrine release disorder, a gastrointestinal disorder,
CC irritable bowel syndrome, a cardiovascular disorder, an electrolyte
CC balance disorder, diuresis, hypertension, hypotension, diabetes,
CC hypoglycemia, a respiratory disorder, asthma, a reproductive function
CC disorder, an immune disorder, an endocrine disorder, a musculoskeletal
CC disorder, a neuroendocrine disorder, a cognitive disorder, a memory
CC disorder, a sensory modulation and transmission disorder, a motor
CC coordination disorder, a sensory integration disorder, obesity, pain,
CC psychotic behaviour, morphine tolerance, nicotine addiction, opiate
CC addiction, affective disorder or migraine (all claimed)
XX
SQ Sequence 1302 BP; 381 A; 303 C; 263 G; 355 T; 0 U; 0 Other;

Query Match 5.2%; Score 61.6; DB 3; Length 1302;
Best Local Similarity 46.3%; Pred. No. 8e-08;
Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

Qy 165 ATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGG 224

```
Db        165 AGCAATCTTCATTATTTCCTACTTTCTGATCTTCTTTTTGTGCATGATGGGAAATACTGT 224

Qy        225 CGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT 284

Db        225 GGTTTGCTTTATTGTAATGAGGAACAAACATATGCACACAGTCACTAATCTCTTCATCTT 284

Qy        285 CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTA 344

Db        285 AAACCTGGCCATAAGTGATTTACTAGTTGGCATATTCTGCATGCCTATAACACTGCTGGA 344

Qy        345 CGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAA 404

Db        345 CAATATTATAGCAGGATGGCCATTTGGAAACACGATGTGCAAGATCAGTGGATTGGTCCA 404

Qy        405 TTCGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCT 464

Db        405 GGGAATATCTGTCGCAGCTTCAGTCTTTACGTTAGTTGCAATTGCTGTAGATAGGTTCCA 464

Qy        465 GCATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATT 524

Db        465 GTGTGTGGTCTACCCTTTTAAACCAAAGCTCACTATCAAGACAGCGTTTGTCATTATTAT 524

Qy        525 TCTTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGT 584

Db        525 GATCATCTGGGTCCTAGCCATCACCATTATGTCTCCATCTGCAGTAATGTTACATGTGCA 584

Qy        585 CGATGGAAGCTTTTAC 600

Db        585 AGAAGAAAAATATTAC 600
```

RESULT 11
ADL32476
ID ADL32476 standard; cDNA; 1302 BP.
XX
AC ADL32476;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human neuropeptide FF receptor (hNPFF2b), cDNA.
XX
KW ss; gene; neuropeptide FF receptor; interstitial cystitis;
KW steroid hormone disorder; gastrointestinal disorder; hypotension;
KW diabetes; hypertension; hypoglycaemia; reproductive function disorder;
KW obesity; morphine tolerance; cognitive disorder; immune disorder;
KW irritable bowel syndrome; migraine; cardiovascular disorder;
KW memory disorder; motor integration disorder; human; NPFF.
XX
OS Homo sapiens.
XX
PN US6709831-B1.
XX
PD 23-MAR-2004.
XX
PF 24-SEP-1999; 99US-00405558.
XX
PR 25-SEP-1998; 98US-00161113.
PR 22-FEB-1999; 99US-00255368.
XX
PA (SYNA-) SYNAPTIC PHARM CORP.
XX
PI Gerald CPG, Jones KA, Bonini JA, Borowsky BE, Craig DA;
XX
DR WPI; 2004-292968/27.
DR P-PSDB; ADL32477.
XX
PT Competitive binding for identifying chemical compound binding to human
PT Neuropeptide FF receptor, comprises contacting cells with chemical
PT compound and second compound and detecting compound binding to receptor.
XX
PS Disclosure; SEQ ID NO 5; 96pp; English.
XX
CC The invention relates to isolated nucleic acids encoding neuropeptide FF
CC (NPFF) receptors. Also described is a method involving competitive
CC binding for identifying a chemical compound which specifically binds to
CC human Neuropeptide FF (NPFF2) receptor. The compound identified by the
CC method is useful for treating interstitial cystitis, steroid hormone
CC disorder, gastrointestinal disorder, hypotension, diabetes, hypertension,
CC hypoglycaemia, reproductive function disorder, obesity, morphine
CC tolerance, cognitive disorder, immune disorder, irritable bowel syndrome,
CC migraine, cardiovascular disorder, memory disorder and motor integration
CC disorder. The present sequence represents cDNA encoding human
CC neuropeptide FF receptor, hNPFF2b.
XX
SQ Sequence 1302 BP; 381 A; 303 C; 263 G; 355 T; 0 U; 0 Other;

```
  Query Match             5.2%;  Score 61.6;  DB 12;  Length 1302;
  Best Local Similarity   46.3%;  Pred. No. 8e-08;
  Matches  202;  Conservative    0;  Mismatches  234;  Indels    0;  Gaps    0;

Qy        165 ATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGG 224

Db        165 AGCAATCTTCATTATTTCCTACTTTCTGATCTTCTTTTTGTGCATGATGGGAAATACTGT 224

Qy        225 CGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT 284

Db        225 GGTTTGCTTTATTGTAATGAGGAACAAACATATGCACACAGTCACTAATCTCTTCATCTT 284

Qy        285 CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTA 344

Db        285 AAACCTGGCCATAAGTGATTTACTAGTTGGCATATTCTGCATGCCTATAACACTGCTGGA 344

Qy        345 CGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAA 404

Db        345 CAATATTATAGCAGGATGGCCATTTGGAAACACGATGTGCAAGATCAGTGGATTGGTCCA 404

Qy        405 TTCGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCT 464

Db        405 GGGAATATCTGTCGCAGCTTCAGTCTTTACGTTAGTTGCAATTGCTGTAGATAGGTTCCA 464

Qy        465 GCATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATT 524

Db        465 GTGTGTGGTCTACCCTTTTAAACCAAAGCTCACTATCAAGACAGCGTTTGTCATTATTAT 524

Qy        525 TCTTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGT 584

Db        525 GATCATCTGGGTCCTAGCCATCACCATTATGTCTCCATCTGCAGTAATGTTACATGTGCA 584

Qy        585 CGATGGAAGCTTTTAC 600

Db        585 AGAAGAAAAATATTAC 600
```

RESULT 12
ADW80001
ID ADW80001 standard; DNA; 1302 BP.
XX
AC ADW80001;
XX
DT 07-APR-2005 (first entry)
XX
DE Human neuropeptide FF2 (NPFF2) receptor protein encoding DNA.
XX
KW DNA purification; gene therapy; screening; transgenic;
KW cardiovascular-gen; cns-gen; hypertensive; hypotensive; diuretic;
KW anorectic; anabolic; eating-disorders-gen; nootropic; antidepressant;
KW neuroleptic; analgesic; gynecological; antidiarrheic;
KW gastrointestinal-gen; genitourinary disease; cardiovascular disease;
KW mood disorder; psychiatric disorder; neurological disease;
KW gastrointestinal disease; neuropeptide FF2 receptor; NPFF2 receptor; ds;
KW gene.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers

```
FT   CDS             31. .1293
FT                   /*tag= a
FT                   /product= "Human neuropeptide FF2 (NPFF2) receptor
FT                   protein"
XX
PN   US6849727-B1.
XX
PD   01-FEB-2005.
XX
PF   29-MAR-2000; 2000US-00538036.
XX
PR   25-SEP-1998;   98US-00161113.
PR   22-FEB-1999;   99US-00255368.
PR   24-SEP-1999;   99US-00405558.
XX
PA   (LUND ) LUNDBECK AS H.
XX
PI   Gerald CPG,  Jones KA,  Bonini JA,  Borowsky BE,  Craig DA;
XX
DR   WPI; 2005-129971/14.
DR   P-PSDB; ADW80002.
XX
PT   New nucleic acid encoding a human or rat neuropeptide FF2 receptor,
PT   useful for diagnosing or treating a disorder, e.g. cardiovascular,
PT   affective, reproductive, gastrointestinal, or lower urinary tract
PT   disorders.
XX
PS   Disclosure; SEQ ID NO 5; 95pp; English.
XX
CC   The present invention relates to a neuropeptide FF (NPFF) receptor
CC   proteins and their DNA. The invention is useful for diagnosing or
CC   treating a disorder, e.g. diuresis, cardiovascular conditions such as
CC   hypertension, hypotension and congestive heart failure, memory loss,
CC   affective disorders, schizophrenia, pain, locomotor problems, circadian
CC   rhythm disorders, eating/body weight disorders, sexual/reproductive
CC   disorders, nasal congestion, diarrhea, gastrointestinal disorders, or
CC   disorders of the lower urinary tract. The invention is also useful in
CC   gene therapy. The present sequence is the human neuropeptide FF2 (NPFF2)
CC   receptor protein encoding DNA.
XX
SQ   Sequence 1302 BP; 381 A; 303 C; 263 G; 355 T; 0 U; 0 Other;

  Query Match             5.2%;  Score 61.6;  DB 14;  Length 1302;
  Best Local Similarity   46.3%;  Pred. No. 8e-08;
  Matches  202;  Conservative    0;  Mismatches  234;  Indels    0;  Gaps    0;

Qy        165 ATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGG 224
              | |||||||||    |   ||||    |  | ||  | ||  |||| | |||||    |
Db        165 AGCAATCTTCATTATTTCCTACTTTCTGATCTTCTTTTTGTGCATGATGGGAAATACTGT 224

Qy        225 CGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT 284
               ||     |    ||   ||| ||||| |   | ||  | |      ||  | ||  |  |
Db        225 GGTTTGCTTTATTGTAATGAGGAACAAACATATGCACACAGTCACTAATCTCTTCATCTT 284

Qy        285 CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTA 344
               ||| ||  | | |  |||||  || | |    |         || ||  | ||||    | |
Db        285 AAACCTGGCCATAAGTGATTTACTAGTTGGCATATTCTGCATGCCTATAACACTGCTGGA 344

Qy        345 CGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAA 404
              |   || |    ||  ||| |||| ||       |||||||  |   |    |   |||    |
Db        345 CAATATTATAGCAGGATGGCCATTTGGAAACACGATGTGCAAGATCAGTGGATTGGTCCA 404

Qy        405 TTCGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCT 464
                  || ||    |   |    |  |   |   ||||||  |  ||||||  || |
Db        405 GGGAATATCTGTCGCAGCTTCAGTCTTTACGTTAGTTGCAATTGCTGTAGATAGGTTCCA 464

Qy        465 GCATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATT 524
              |  |  |   | | ||    |||| |    |  ||||       ||||||  |  || |   |
Db        465 GTGTGTGGTCTACCCTTTTAAACCAAAGCTCACTATCAAGACAGCGTTTGTCATTATTAT 524

Qy        525 TCTTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGT 584
                | |||||| |  |  | |    || |    || | |    |   ||  |
Db        525 GATCATCTGGGTCCTAGCCATCACCATTATGTCTCCATCTGCAGTAATGTTACATGTGCA 584

Qy        585 CGATGGAAGCTTTTAC 600
                ||  | ||  | ||||
Db        585 AGAAGAAAAATATTAC 600


RESULT 13
ADZ76145
ID   ADZ76145 standard; DNA; 1302 BP.
XX
AC   ADZ76145;
XX
DT   14-JUL-2005  (first entry)
XX
DE   Human neuropeptide FF receptor (NPFF2b) DNA, SEQ ID NO: 5.
XX
KW   Neuropeptide FF receptor; urinary tract disease; uropathic;
KW   antiinflammatory; genitourinary disease; gastrointestinal disease;
KW   gastrointestinal-gen.; cardiovascular disease; cardiovascular-gen.;
KW   hypotensive; hypertensive; antidiabetic; metabolic disorder;
KW   respiratory disease; respiratory-gen.; antiasthmatic; inflammation;
KW   genitourinary disease; immune disorder; immunomodulator;
KW   endocrine disease; endocrine-gen.; musculoskeletal disease;
KW   muscular-gen.; osteopathic; cognitive disorder; nootropic;
KW   neurological disease; memory disorder; anorectic; nutritional disorder;
KW   analgesic; antismoking; psychiatric disorder; toxicity and intoxication;
KW   antiaddictive; antimigraine; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             31. .1293
FT                   /*tag= a
FT                   /product= "Human NPFF receptor (NPFF2b) protein"
XX
PN   US2005089937-A1.
XX
PD   28-APR-2005.
XX
PF   18-NOV-2004; 2004US-00992407.
XX
PR   25-SEP-1998;   98US-00161113.
PR   22-FEB-1999;   99US-00255368.
PR   24-SEP-1999;   99US-00405558.
PR   29-MAR-2000; 2000US-00538036.
XX
PA   (GERA/) GERALD C P G.
PA   (JONE/) JONES K A.
PA   (BONI/) BONINI J A.
PA   (BORO/) BOROWSKY B E.
PA   (CRAI/) CRAIG D A.
XX
PI   Gerald CPG,  Jones KA,  Bonini JA,  Borowsky BE,  Craig DA;
XX
DR   WPI; 2005-344283/35.
DR   P-PSDB; ADZ76146.
XX
PT   Preparing a composition that specifically binds to mammalian neuropeptide
PT   FF (NPFF) receptor, comprises determining if the compound is a mammalian
PT   NPFF receptor agonist, recovering the compound and admixing a carrier.
XX
PS   Disclosure; SEQ ID NO 5; 103pp; English.
XX
CC   The invention relates to a method for preparing a composition that
CC   specifically binds to mammalian neuropeptide FF (NPFF) receptor. The
CC   method involves determining whether the compound is a mammalian NPFF
CC   receptor agonist, recovering the compound and admixing a carrier. The
CC   method is useful for preparing a composition which specifically binds to
CC   mammalian NPFF receptor. The composition is used to treat e.g. a lower
CC   urinary tract disorder such as interstitial cystitis or urinary
CC   incontinence, a gastrointestinal disorder, irritable bowel syndrome, a
CC   cardiovascular disorder, hypertension, hypotension, diabetes,
CC   hypoglycemia, a respiratory disorder, asthma, a reproductive function
```

CC disorder, an immune disorder, an endocrine disorder, a musculoskeletal
CC disorder, a cognitive disorder, a memory disorder, obesity, pain,
CC nicotine addiction, opiate addiction or migraine. The present sequence is
CC the human NPFF receptor (NPFF2b; NPFF2) DNA.
XX
SQ Sequence 1302 BP; 381 A; 303 C; 263 G; 355 T; 0 U; 0 Other;

Query Match 5.2%; Score 61.6; DB 14; Length 1302;
Best Local Similarity 46.3%; Pred. No. 8e-08;
Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

```
Qy       165 ATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGG 224
            | |||||||||   |   ||||   |  | ||  | ||  ||||  | |||||    |
Db       165 AGCAATCTTCATTATTTCCTACTTTCTGATCTTCTTTTTGTGCATGATGGGAAATACTGT 224

Qy       225 CGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT 284
             ||    |     ||   ||| ||||| |   | ||  | |     ||  | ||  |  |
Db       225 GGTTTGCTTTATTGTAATGAGGAACAAACATATGCACACAGTCACTAATCTCTTCATCTT 284

Qy       285 CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTA 344
             ||| ||  | | |  |||||  || | |  |        || ||  | ||||    | |
Db       285 AAACCTGGCCATAAGTGATTTACTAGTTGGCATATTCTGCATGCCTATAACACTGCTGGA 344

Qy       345 CGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAA 404
             |   || |    ||  ||| |||| ||       |||||| |  |   |   |||    |
Db       345 CAATATTATAGCAGGATGGCCATTTGGAAACACGATGTGCAAGATCAGTGGATTGGTCCA 404

Qy       405 TTCGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCT 464
                || ||    |   |     |  |   |  |||||  |  |||||  || |
Db       405 GGGAATATCTGTCGCAGCTTCAGTCTTTACGTTAGTTGCAATTGCTGTAGATAGGTTCCA 464

Qy       465 GCATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATT 524
             |  | |   | | ||    |||| |   |  ||||      |||||| |  || |   |
Db       465 GTGTGTGGTCTACCCTTTAAACCAAAGCTCACTATCAAGACAGCGTTTGTCATTATTAT 524

Qy       525 TCTTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGT 584
              | ||||||  |  |  | |     || |    || | |     |    ||  |
Db       525 GATCATCTGGGTCCTAGCCATCACCATTATGTCTCCATCTGCAGTAATGTTACATGTGCA 584

Qy       585 CGATGGAAGCTTTTAC 600
             || | ||  | ||||
Db       585 AGAAGAAAAATATTAC 600
```

RESULT 14
AAA57839
ID AAA57839 standard; DNA; 1440 BP.
XX
AC AAA57839;
XX
DT 20-OCT-2000 (first entry)
XX
DE DNA encoding a human A4 receptor polypeptide.
XX
KW Human; G protein coupled receptor; A4 receptor; cell line; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 121. .1383
FT /*tag= a
FT /product= "A4 receptor"
XX
PN CA2284857-A1.
XX
PD 16-APR-2000.
XX
PF 15-OCT-1999; 99CA-02284857.
XX
PR 16-OCT-1998; 98US-00104514.
PR 16-OCT-1998; 98US-00173565.
XX
PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
XX
PI Zastawny RL;
XX
DR WPI; 2000-491457/44.
DR P-PSDB; AAB07426.
XX
PT Novel polynucleotide encoding G protein coupled receptor A4, useful for
PT producing recombinant cell lines for discovering therapeutic agents that
PT modulate the receptor activity.
XX
PS Claim 2; Fig 1; 59pp; English.
XX
CC The present sequence encodes a human G protein coupled receptor A4. The
CC A4 polynucleotide is found in adult human kidney, liver, lung, and
CC placenta. The receptor shows homology to the orexin receptor family. The
CC A4 polynucleotide sequence is useful for producing recombinant cell lines
CC that have commercial significance in discovering therapeutic compounds
CC that modulate the receptor activity
XX
SQ Sequence 1440 BP; 415 A; 334 C; 300 G; 391 T; 0 U; 0 Other;

Query Match 5.2%; Score 61.6; DB 3; Length 1440;
Best Local Similarity 46.3%; Pred. No. 8.4e-08;
Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

```
Qy       165 ATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGG 224
            | |||||||||   |   ||||   |  | ||  | ||  ||||  | |||||    |
Db       255 AGCAATCTTCATTATTTCCTACTTTCTGATCTTCTTTTTGTGCATGATGGGAAATACTGT 314

Qy       225 CGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT 284
             ||    |     ||   ||| ||||| |   | ||  | |     ||  | ||  |  |
Db       315 GGTTTGCTTTATTGTAATGAGGAACAAACATATGCACACAGTCACTAATCTCTTCATCTT 374

Qy       285 CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTA 344
             ||| ||  | | |  |||||  || | |  |        || ||  | ||||    | |
Db       375 AAACCTGGCCATAAGTGATTTACTAGTTGGCATATTCTGCATGCCTATAACACTGCTGGA 434

Qy       345 CGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAA 404
             |   || |    ||  ||| |||| ||       |||||| |  |   |   |||    |
Db       435 CAATATTATAGCAGGATGGCCATTTGGAAACACGATGTGCAAGATCAGTGGATTGGTCCA 494

Qy       405 TTCGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCT 464
                || ||    |   |     |  |   |  |||||  |  |||||  || |
Db       495 GGGAATATCTGTCGCAGCTTCAGTCTTTACGTTAGTTGCAATTGCTGTAGATAGGTTCCA 554

Qy       465 GCATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATT 524
             |  | |   | | ||    |||| |   |  ||||      |||||| |  || |   |
Db       555 GTGTGTGGTCTACCCTTTAAACCAAAGCTCACTATCAAGACAGCGTTTGTCATTATTAT 614

Qy       525 TCTTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGT 584
              | ||||||  |  |  | |     || |    || | |     |    ||  |
Db       615 GATCATCTGGGTCCTAGCCATCACCATTATGTCTCCATCTGCAGTAATGTTACATGTGCA 674

Qy       585 CGATGGAAGCTTTTAC 600
             || | ||  | ||||
Db       675 AGAAGAAAAATATTAC 690
```

RESULT 15
ACH00816
ID ACH00816 standard; DNA; 1560 BP.
XX
AC ACH00816;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human neuropeptide FF 2 coding sequence.
XX
KW Energy homeostasis; mouse; metabolism; triglyceride; metabolic disease;
KW gene therapy; anorectic; immunomodulator; antidiabetic; hypotensive;
KW cardiant; osteopathic; antilipemic; gene; ds.
XX
OS Homo sapiens.

XX
PN WO2003075945-A2.
XX
PD 18-SEP-2003.
XX
PF 14-MAR-2003; 2003WO-EP002714.
XX
PR 14-MAR-2002; 2002EP-00005882.
PR 15-MAR-2002; 2002EP-00006012.
PR 20-MAR-2002; 2002EP-00006271.
PR 25-MAR-2002; 2002EP-00006810.
XX
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
XX
PI Eulenberg K, Steuernagel A, Haeder T, Broenner G;
XX
DR WPI; 2003-748334/70.
DR P-PSDB; ABG75056.
XX
PT New pharmaceutical composition comprising a nucleic acid molecule
PT encoding proteins regulating the energy homeostasis and metabolism of
PT triglycerides useful for detecting or preventing metabolic diseases, e.g.
PT obesity.
XX
PS Claim 2; Fig 7B; 140pp; English.
XX
CC The present invention relates to pharmaceutical compositions comprising
CC the coding sequences shown in ACH00815-ACH00827, or their encoded
CC proteins (shown in ABG75054, ABG75056-ABG75067). These are proteins
CC involved in the metabolism of triglycerides and in energy homeostasis,
CC and their coding sequences. The composition is useful for the manufacture
CC of an agent for detecting, verifying, treating, alleviating or preventing
CC disorders, including metabolic diseases such as obesity and other body-
CC weight regulation disorders as well as related disorders such as
CC metabolic syndrome, eating disorder, cachexia, diabetes mellitus,
CC hypertension, coronary heart disease, hypercholesterolaemia,
CC dyslipidaemia, osteoarthritis or gallstones, in cells, cell masses,
CC organs or subjects. The coding sequences can be used in the production of
CC transgenic animals which under- or over-produce the gene of interest. The
CC present sequence is a coding sequence of the invention
XX
SQ Sequence 1560 BP; 476 A; 347 C; 287 G; 450 T; 0 U; 0 Other;

Query Match 5.2%; Score 61.6; DB 10; Length 1560;
Best Local Similarity 46.3%; Pred. No. 8.7e-08;
Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

```
Qy        165 ATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGG 224
              | |||||||||    |   ||||    |  | ||  | ||  ||||  | |||||    |
Db        182 AGCAATCTTCATTATTTCCTACTTTCTGATCTTCTTTTTGTGCATGATGGGAAATACTGT 241

Qy        225 CGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT 284
              ||    |    ||   ||| ||||| |    | ||  | |      ||  | ||  |  |
Db        242 GGTTTGCTTTATTGTAATGAGGAACAAACATATGCACACAGTCACTAATCTCTTCATCTT 301

Qy        285 CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTA 344
               ||| ||  | | |  |||||  || | |   |       || ||  | ||||    | |
Db        302 AAACCTGGCCATAAGTGATTTACTAGTTGGCATATTCTGCATGCCTATAACACTGCTGGA 361

Qy        345 CGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAA 404
              |   || |    ||  ||| |||| ||       |||||| |  |   |   |||    |
Db        362 CAATATTATAGCAGGATGGCCATTTGGAAACACGATGTGCAAGATCAGTGGATTGGTCCA 421

Qy        405 TTCGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCT 464
                || ||   |  |   |  |  |   |  |||||  |  ||||||  || |
Db        422 GGGAATATCTGTCGCAGCTTCAGTCTTTACGTTAGTTGCAATTGCTGTAGATAGGTTCCA 481

Qy        465 GCATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATT 524
              |  | |   | | ||    |||| |    |  ||||      ||||||  |  || |   |
Db        482 GTGTGTGGTCTACCCTTTTAAACCAAAGCTCACTATCAAGACAGCGTTTGTCATTATTAT 541

Qy        525 TCTTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGT 584
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Db        542 GATCATCTGGGTCCTAGCCATCACCATTATGTCTCCATCTGCAGTAATGTTACATGTGCA 601

Qy        585 CGATGGAAGCTTTTAC 600
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Search completed: May 8, 2006, 14:50:30
Job time : 815 secs

GenCore version 5.1.8

OM nucleic - nucleic search, using sw model

Run on: May 8, 2006, 14:37:08 ; Search time 1118 Seconds
(without alignments)
8824.122 Million cell updates/sec

Title: US-10-650-467-104
Perfect score: 1193
Sequence: 1 atggttagttcggcggccac.....tgtgcaggcaactctttcta 1193

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1193	100.0	1193	9	US-10-650-467-104	Sequence 104, App
2	1193	100.0	1500	9	US-10-650-467-39	Sequence 39, Appl
3	1109	93.0	1301	9	US-10-650-467-106	Sequence 106, App
4	96.6	8.1	1130	9	US-10-650-467-21	Sequence 21, Appl
5	84	7.0	1098	9	US-10-650-467-35	Sequence 35, Appl
6	78.8	6.6	1352	9	US-10-650-467-15	Sequence 15, Appl
7	66.6	5.6	1374	9	US-10-650-467-25	Sequence 25, Appl
8	61.6	5.2	1302	3	US-09-866-248A-5	Sequence 5, Appli
9	61.6	5.2	1302	9	US-10-992-407-5	Sequence 5, Appli
10	61.6	5.2	1400	10	US-11-060-756-2491	Sequence 2491, Ap
11	61.6	5.2	1400	10	US-11-060-756-6763	Sequence 6763, Ap
12	61.6	5.2	1440	6	US-10-060-369-8	Sequence 8, Appli
13	61.6	5.2	1560	9	US-10-507-617-4	Sequence 4, Appli
14	61.6	5.2	1560	9	US-10-949-140-1	Sequence 1, Appli
15	61.6	5.2	1824	7	US-10-276-774-743	Sequence 743, App
16	61.6	5.2	1936	5	US-10-225-567A-511	Sequence 511, App
17	61.6	5.2	1936	6	US-10-255-551-1	Sequence 1, Appli
18	61.6	5.2	1936	7	US-10-283-975A-399	Sequence 399, App
19	61.6	5.2	1936	8	US-10-757-262-7	Sequence 7, Appli
20	61.6	5.2	1936	8	US-10-723-860-4147	Sequence 4147, Ap
21	61.6	5.2	1938	8	US-10-723-860-8018	Sequence 8018, Ap
22	60.2	5.0	1557	3	US-09-804-551B-7	Sequence 7, Appli
23	60.2	5.0	1803	6	US-10-283-423-1	Sequence 1, Appli
24	60.2	5.0	1803	6	US-10-213-821-1	Sequence 1, Appli
25	60.2	5.0	1803	7	US-10-736-048-1	Sequence 1, Appli
26	60.2	5.0	1803	8	US-10-489-425-61	Sequence 61, Appl
27	60.2	5.0	2504	10	US-11-097-143-41471	Sequence 41471, A
28	60.2	5.0	16870	10	US-11-097-143-41470	Sequence 41470, A
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31	57.8	4.8	1401	7	US-10-181-906-5	Sequence 5, Appli
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36	57.8	4.8	1605	6	US-10-291-446-1	Sequence 1, Appli
37	57.8	4.8	1605	6	US-10-305-720-1231	Sequence 1231, Ap
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39	57.8	4.8	1605	8	US-10-705-446-1	Sequence 1, Appli
40	57.8	4.8	1605	8	US-10-926-225-1	Sequence 1, Appli
41	57.8	4.8	1605	8	US-10-415-457-3	Sequence 3, Appli
42	57.8	4.8	1605	10	US-11-029-242-1	Sequence 1, Appli
43	57.8	4.8	1888	5	US-10-176-847-25	Sequence 25, Appl
44	57.8	4.8	2624	6	US-10-017-273A-2	Sequence 2, Appli
45	57.8	4.8	2624	8	US-10-686-390-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-10-650-467-104
; Sequence 104, Application US/10650467
; Publication No. US20050176069A1
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Geary, Timothy G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/10/650,467
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/721,870
; PRIOR FILING DATE: CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 104
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1191)
; FEATURE:
; OTHER INFORMATION: Clone identifier: CEGPCR19.2
US-10-650-467-104

Query Match 100.0%; Score 1193; DB 9; Length 1193;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 60

Qy         61 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120

Qy        121 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 180
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Db        121 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 180

Qy        181 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 240
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Db        181 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 240

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Db        241 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 300

Qy        301 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 360

Qy        361 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 420
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Db        361 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 420

Qy        421 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC 480
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Db        421 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC 480

Qy        481 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 540
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Db        541 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC 600

Qy        601 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 660
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Db        601 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 660

Qy        661 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 720
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Qy        721 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 780
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900

Qy        901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960
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Db       1141 GACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 1193


RESULT 2
US-10-650-467-39
; Sequence 39, Application US/10650467
; Publication No. US20050176069A1
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Geary, Timothy G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 28341/6223
;  CURRENT APPLICATION NUMBER: US/10/650,467
;  CURRENT FILING DATE:  2003-08-28
;  PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/721,870
;  PRIOR FILING DATE: CURRENT FILING DATE:  2000-11-24
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
;   LENGTH: 1500
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1497)
;   FEATURE:
;   OTHER INFORMATION: Clone identifier: CEGPCR19
US-10-650-467-39

  Query Match            100.0%;  Score 1193;  DB 9;  Length 1500;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1193;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        241 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 300
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Db        547 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 606

Qy        301 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 360
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Qy        361 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 420
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Db        667 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 726

Qy        421 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC 480
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Db        727 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC 786

Qy        481 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 540
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Db        787 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 846

Qy        541 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC 600
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Qy        601 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 660
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Db        907 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 966

Qy        661 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 720
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Db        967 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 1026
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Qy        721 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 780
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Db       1027 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 1086

Qy        781 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 1146

Qy        841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 1206

Qy        901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960
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Db       1207 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 1266

Qy        961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020
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Db       1267 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1326

Qy       1021 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1080
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Db       1327 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1386

Qy       1081 AACTCAACAGAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAGGGATCCAGCTACAC 1140
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Db       1387 AACTCAACAGAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAGGGATCCAGCTACAC 1446

Qy       1141 GACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 1193
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Db       1447 GACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 1499
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RESULT 3
US-10-650-467-106
; Sequence 106, Application US/10650467
; Publication No. US20050176069A1
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Geary, Timothy G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/10/650,467
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/721,870
; PRIOR FILING DATE: CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 106
; LENGTH: 1301
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1299)
; FEATURE:
; OTHER INFORMATION: Clone identifier: CEGPCR19.1
US-10-650-467-106

Query Match 93.0%; Score 1109; DB 9; Length 1301;
Best Local Similarity 94.2%; Pred. No. 0;
Matches 1193; Conservative 0; Mismatches 0; Indels 74; Gaps 1;

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Qy          1 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 60

Qy         61 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120

Qy        121 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 180

Qy        181 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 240

Qy        241 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 300

Qy        301 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 360

Qy        361 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 420

Qy        421 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC 480

Qy        481 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 540

Qy        541 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC 600

Qy        601 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 660

Qy        661 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 720

Qy        721 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 780

Qy        781 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 840

Qy        841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900

Qy        901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960

Qy        961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020

Qy       1021 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1080

Qy       1081 AACTCAACAG---------------------------------------------------- 1090
              ||||||||||
Db       1081 AACTCAACAGAGATTGTGTCCTCGTTTGCCAGTAGAGTGAGTAACTCGATTCGGCGGTCA 1140

Qy       1091 ----------------------AGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAG 1126
                                     ||||||||||||||||||||||||||||||||||||
Db       1141 ACGTTTCGGAGAAACAATATTGACAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAG 1200
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Qy       1127 GGATCCAGCTACACGACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACT 1186
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGATCCAGCTACACGACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACT 1260

Qy       1187 CTTTCTA 1193
             |||||||
Db       1261 CTTTCTA 1267
```

RESULT 4
US-10-650-467-21
; Sequence 21, Application US/10650467
; Publication No. US20050176069A1
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Geary, Timothy G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/10/650,467
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/721,870
; PRIOR FILING DATE: CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 1130
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1128)
; FEATURE:
; OTHER INFORMATION: Clone identifier: CEGPCR4
US-10-650-467-21

Query Match 8.1%; Score 96.6; DB 9; Length 1130;
Best Local Similarity 47.0%; Pred. No. 2.1e-18;
Matches 438; Conservative 0; Mismatches 454; Indels 39; Gaps 3;

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Qy        136 GATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCCTG 195
              || ||| |  |   |   |  |||||    | | | ||  |||| ||||||  | |  |
Db         52 GAAGATTTGTCATCAAGGTGGTACATAATGTTAGTGTTTGCATTTCTCTACCTGATAATC 111

Qy        196 TTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAAACAAGCGG 255
               |||     || ||  |||||||||    | ||  | | |||  |  | || |||||
Db        112 ATTGCCGCCGGAATAATTGGAAACTCATGTGTGATTTTGGCAATCACAAGGAACAAATCA 171

Qy        256 CTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATATTGGTG 315
              || ||| | | ||  ||  | ||| | ||    ||    |  | ||| |  |  |
Db        172 CTTCAAACTGTTCCGAATCTGTTTATTCTTTCTTTATCATGTTCTGATATTGTGGTATGC 231

Qy        316 TTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGACTGGGCATTCGGGTCA 375
              | |||| |     || |||| ||        ||  | |  ||||| |||   || ||
Db        232 TGCACATCTGCAACAATCACTCCGATTACTGCATTCAAGAAAGAATGGATCTTTGGAGAG 291

Qy        376 GTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTTGTGACGAGTTGGAGC 435
              |  | ||||   | ||  || ||        |       | | | |  | | ||  |
Db        292 GCTTTATGCCGAATTGCACCATTCATTGCTGGTATCAGCCTTTGTTTCTCAACTTTCACA 351

Qy        436 CTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCCACCAAACAACCAGTT 495
              | ||||||||||||| | || | ||   | |  ||     ||| |  |  ||||  ||
Db        352 TTGACTGCAATCTCCATCGACAGATACATCCTGATTCGATTTCCGATGAGGAAACCTATT 411

Qy        496 TCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTCTCAACACTGATAAAT 555
              |    |  ||||||| | | | | |    | |||| ||      |  |  ||   || |
Db        412 ACGCATTATCAAGCGGTTGGAGTGATTGCTATTATTTGCGCTTTTGCTGCAACCATCA-- 469

Qy        556 CTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTACGTTCAGCCCGGAGAA 615
              |  |  |  ||    ||| ||||       |||   ||| |   |
Db        470 ----CATCCCCAATAATGTTCAAGCAAAAGCTGGGAGAGTTTGAGAAT----------- 513
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Qy        616 ACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGCGAAAATAGTCGAAAG 675
                  |  || ||||| |  |||   ||         |    | ||||      ||||
Db        514 ------TTTTGTGGGCAGTACTGCACGGAAAACTGGGGAGCCAATGAAAGCCAGAGAAAA 567

Qy        676 ATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATGGCAGTGATCACGTAT 735
              ||||| ||  |  | | ||||  | ||| ||||| | ||| |  |  | ||||
Db        568 ATTTATGGTGCAGCTCTGATGTTTCTTCAGCTCGTCATTCCGCTTACCATCATCATCATA 627

Qy        736 TGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATCCAAAATGCTCAATTC 795
              | ||||      || |    ||  |  | ||  |||||  || ||   ||  ||
Db        628 TCCTACACTGCGATTTCTTTGAAGATCGGACAAAGCATGATTCTCAAAGGGGCGAAAAAG 687

Qy        796 TGTCAATCACTGA--------------CACAAAAGCAGAGAAGTGATGCGACGTCACGA 840
                || ||  |                |    | |||   |||    ||   |    ||
Db        688 CAAAAAACAGACAATTGGGAAATGGAATTAAGTGATCAACAAAGAATCGCTGTGAAGAGA 747

Qy        841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900
              |  | | |   |||   || || ||||  ||||| ||| ||||      |  | ||| |
Db        748 AGACAAAGAACTAATAGAATGCTTATTGGTATGGTAGTCGCATTCGCTTGCAGCTGGATT 807

Qy        901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960
              | |       ||||  |  | |  || | || |  ||| ||      | |||  |
Db        808 TGGTCAGTGACGTTCAACATTCTGAGGGACTATGAATATTTGCCAGAGCTCATCAAAACT 867

Qy        961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020
              ||     |   ||| | |||   | | ||   ||| || ||| ||| |   || ||||||
Db        868 CAAGAATATATCTTTGGAATTGCTACACATTGCATTGCAATGACCTCAACGGTATGGAAC 927

Qy       1021 CCTCTGCTATTCTTTTGGCTGACACGAAAAC 1051
              ||  | || | |     ||| |  |   |||
Db        928 CCGTTACTCTACGCAGTGCTCAACCTCCAAC 958
```

RESULT 5
US-10-650-467-35
; Sequence 35, Application US/10650467
; Publication No. US20050176069A1
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Geary, Timothy G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/10/650,467
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/721,870
; PRIOR FILING DATE: CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 1098
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1095)
; FEATURE:
; OTHER INFORMATION: Clone identifier: CEGPCR16
US-10-650-467-35

Query Match 7.0%; Score 84; DB 9; Length 1098;
Best Local Similarity 50.5%; Pred. No. 1.6e-14;
Matches 204; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

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Qy        167 CAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCG 226
              | |||  |  ||  | |||||     |  |  | |||  | |||  |     || ||       |
Db         86 CGATTCTTGCAACCATCTACACTATAATTGTCGTAGTTGGCGTAACCGGCAATTTGTTAG 145

Qy        227 TACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCA 286
              || |   | |||||  |||   |||    || ||||| |   | ||| | ||  |  |
Db        146 TAGTGATGTCGGTGATGAGGTTCAAAGTTCTTCAATCAGTCAGGAACATGTTCATCGTAT 205
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Qy        287 ACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACG 346
              |||    |  | ||  |  |  ||| | |     | |||| || ||        ||
Db        206 CTTTGTCAGTTTCTGACATTTTTGTGGCGATTGTTAGTGGTTCAGTAACGCCGATAACCG 265

Qy        347 CGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATT 406
              |  |  |||| |||  ||| ||    |    |||| |||||| | ||||||| | |
Db        266 CATTCTCTAAAGTTTGGTTATTTGGTGGACCATTGTGTCATTTACTACCTTTGTTACAGG 325

Qy        407 CGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGC 466
              || ||  | | | | | |  ||||| |||||  |  | || | || | | |
Db        326 GTACCGCGTTGAGTTTTTCCACGTTAACGCTCACCGCAATTGCAATTGACAGATATATTC 385

Qy        467 ATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTC 526
              |||    |||| || ||| |||| |     |    |||||| |||  ||| | |  |
Db        386 TCATCTGTCATCCGACGAAAGAACCGATACGCAAAGATCAAGCATTGAAAATGATAAGTT 445

Qy        527 TTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATG 570
              | | | |    |||||  | |    |||| |   | |||
Db        446 TCAACAGCGCCATCTCAGTTGGGCTTTCGGTACCATTATTCATG 489


RESULT 6
US-10-650-467-15
; Sequence 15, Application US/10650467
; Publication No. US20050176069A1
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Geary, Timothy G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 28341/6223
;  CURRENT APPLICATION NUMBER: US/10/650,467
;  CURRENT FILING DATE:  2003-08-28
;  PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/721,870
;  PRIOR FILING DATE: CURRENT FILING DATE:  2000-11-24
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 1352
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1350)
;   FEATURE:
;   OTHER INFORMATION: Clone identifier: CEGPCR14
US-10-650-467-15

  Query Match             6.6%;  Score 78.8;  DB 9;  Length 1352;
  Best Local Similarity   47.4%;  Pred. No. 7.4e-13;
  Matches  381;  Conservative    0;  Mismatches  402;  Indels   21;  Gaps    4;

Qy        134 TCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCC 193
              || |||||   || ||   |||| |  | ||        |   || | || |||    ||
Db         56 TCAATGATTGGACAGTCCTCTTTGAAGTTCGGCTTGGATATTCAGTACTATACTTTCTCA 115

Qy        194 TGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAAACAAGC 253
              | ||  || | ||  |  |||||||  ||      |  |     |  |  |     |||
Db        116 TATTAATAATCGGATTGGTTGGAAATGGGCTATTGATCACTTCAATTTTAATGCGAAAGA 175

Qy        254 GGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATATTGG 313
              ||      |||    ||| |||| || | ||| ||    |  | ||||||  |  |
Db        176 AACTTTCCGTGGC---AAACATATTCTTGATAAACCTGGCAGTTTCTGATTTGCTTCTTT 232

Qy        314 TGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGACTGGGCATTCGGGT 373
              ||||  ||| | ||  |||| |||    | ||| | |  ||     |||  ||| ||
Db        233 GCATCACGGCGGTGCCGATCACTCCAGTATTGGCGTTTATGAAGCGATGGATATTTGGAA 292

Qy        374 CAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTTGTGACGAGTTGGA 433
              | | |||||  | || |||||     |   ||| |||||||  |  |   |   |||
Db        293 TAATTATGTGTAAATTGGTTCCAACTTGTCAGGCGTTTTCGGTGCTCATTTCTTCATGGT 352

Qy        434 GCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCCACCAAACAACCAG 493
              |    |   ||| |  |||| || ||     |||          ||  |     |||||
Db        353 CTTTGTGTTACATCGCAATTGATAGATATCGAAGTATTGTGACGCCACTCCGGGAACCAT 412

Qy        494 TTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTCTCAACACTGATAA 553
              |||  | | || ||   |      |     |  | |  ||| | |||  |    ||    |
Db        413 GGTCTGATAGGCATGCAAGGTGGCTTCTGATGTTCACATGGGTGGTCGCCTTCCTTGCTA 472

Qy        554 ATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTACGTTCAGCCCGGAG 613
              |    |||| | | | || |    ||   |     ||  |     |  ||  |    |
Db        473 GT------TATCCTCTATATTACTCACAGAACTTGAAAACAATGGTTATTGA------AA 520

Qy        614 AAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGCGAAAATAGTCGAA 673
              |   |||  || ||  | |||||| ||||   |||||||||   ||  | |     |
Db        521 ATGTGACATTATGTGGAGATTTTTGCGGCGAGTTCAATTGGCAGTCGGATGAAATATCCA 580

Qy        674 AGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATGGCAGTGATCACGT 733
              ||  |     ||||||  | | ||| |       |  |       ||| | |||| ||
Db        581 AGTTGACATATACTACGAGTTTATTGATTATTCAGCTGATTATTCCAGCAATTATCATGT 640

Qy        734 ATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATCCAAAATGCTCAAT 793
              ||  | |    ||| | | | ||  | | ||  |       |     | |   ||
Db        641 CTTTTTGTTATTTAATGATTCTACAAAAGGTACAAACCGACTGGCTTGTCGACGAGGGAT 700

Qy        794 TCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGAAAGAAGAAAGTGA 853
              |     |     ||||| ||   ||  |  |     ||||||     |||||
Db        701 CCATGTTGACTGCCGCACAACAGGCTCAAACAGCAG------TTCGAAAGCGACGAGTGA 754

Qy        854 ATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTGCCTTTAACATTAC 913
              ||  |  | |||  ||||||| |     ||||| |  || |||||  || ||  |
Db        755 TGTACGTGTTGATTCTAATGGTTATTGTTTTTATGGCTTGCTGGTTCCCGTTGTCCGCCG 814

Qy        914 TCAATTTGGTCAAAGATTTTAAAA 937
              | ||||||  ||| ||||  |   ||
Db        815 TGAATTTGTTCAGAGATCTCGGAA 838


RESULT 7
US-10-650-467-25
; Sequence 25, Application US/10650467
; Publication No. US20050176069A1
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Geary, Timothy G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 28341/6223
;  CURRENT APPLICATION NUMBER: US/10/650,467
;  CURRENT FILING DATE:  2003-08-28
;  PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/721,870
;  PRIOR FILING DATE: CURRENT FILING DATE:  2000-11-24
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
;   LENGTH: 1374
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1371)
;   FEATURE:
;   OTHER INFORMATION: Clone identifier: CEGPCR7
US-10-650-467-25

  Query Match             5.6%;  Score 66.6;  DB 9;  Length 1374;
  Best Local Similarity   48.3%;  Pred. No. 4.4e-09;
  Matches  186;  Conservative    0;  Mismatches  199;  Indels    0;  Gaps    0;

Qy        180 CCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGT 239
              | | |||   || || ||| |  | ||  | |||||||| |    |  |  |  |
Db         93 CGTGTACCTTTTTCTCTTTTTTCTTGGACTCTTTGGAAATGTGACCTTGATTTACGTAAC 152
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Qy        240 GGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCAC 299
Db        153 TTGCAGCCATAAAGCTTTACTGAGCGTTCAAAACATATTCATTCTGAACCTGGCGGCGAG 212

Qy        300 CGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGA 359
Db        213 CGATTGCATGATGTGCATATTATCGCTTCCAATCACTCCAATCACAAATGTGTACAAAAA 272

Qy        360 CTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTT 419
Db        273 CTGGTACTTTGGAAATCTACTCTGCCATTTGATACCATGCATTCAAGGTATCAGCATTTT 332

Qy        420 TGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCC 479
Db        333 CGTATGCACATTCAGTCTCGGTGCGATTGCTTTGGATCGGTATATCCTTGTAGTAAGACC 392

Qy        480 CACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGT 539
Db        393 ACATTCTACACCACTATCCCAAAGAGGAGCATTTCTTACTACTGTTCTATTGTGGATCCT 452

Qy        540 CTCAACACTGATAAATCTACCGTAT 564
Db        453 CTCTTTTGTTGTAACTCTACCCTAT 477
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RESULT 8
US-09-866-248A-5
; Sequence 5, Application US/09866248A
; Publication No. US20020198367A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: 1795/57155-A
; CURRENT APPLICATION NUMBER: US/09/866,248A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 5
; LENGTH: 1302
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-248A-5

Query Match 5.2%; Score 61.6; DB 3; Length 1302;
Best Local Similarity 46.3%; Pred. No. 1.5e-07;
Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

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Qy        165 ATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGG 224
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Qy        225 CGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT 284
Db        225 GGTTTGCTTTATTGTAATGAGGAACAAACATATGCACACAGTCACTAATCTCTTCATCTT 284

Qy        285 CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTA 344
Db        285 AAACCTGGCCATAAGTGATTTACTAGTTGGCATATTCTGCATGCCTATAACACTGCTGGA 344

Qy        345 CGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAA 404
Db        345 CAATATTATAGCAGGATGGCCATTTGGAAACACGATGTGCAAGATCAGTGGATTGGTCCA 404

Qy        405 TTCGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCT 464
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Qy        465 GCATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATT 524
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Qy        525 TCTTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGT 584
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RESULT 9
US-10-992-407-5
; Sequence 5, Application US/10992407
; Publication No. US20050089937A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; TITLE OF INVENTION: And Uses Thereof
; FILE REFERENCE: 57155-D/JPW
; CURRENT APPLICATION NUMBER: US/10/992,407
; CURRENT FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: US/09/538,036
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/405,558
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 09/255,368
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1302
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-992-407-5

Query Match 5.2%; Score 61.6; DB 9; Length 1302;
Best Local Similarity 46.3%; Pred. No. 1.5e-07;
Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

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Qy        225 CGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT 284
Db        225 GGTTTGCTTTATTGTAATGAGGAACAAACATATGCACACAGTCACTAATCTCTTCATCTT 284

Qy        285 CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTA 344
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Qy        345 CGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAA 404
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Qy        405 TTCGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCT 464
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Qy        465 GCATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATT 524
Db        465 GTGTGTGGTCTACCCTTTTAAACCAAAGCTCACTATCAAGACAGCGTTTGTCATTATTAT 524

Qy        525 TCTTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGT 584
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RESULT 10
US-11-060-756-2491
; Sequence 2491, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2491
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-2491

Query Match 5.2%; Score 61.6; DB 10; Length 1400;
Best Local Similarity 46.3%; Pred. No. 1.6e-07;
Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

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Qy        225 CGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT 284
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Qy        285 CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTA 344
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Qy        345 CGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAA 404
Db        183 CAATATTATAGCAGGATGGCCATTTGGAAACACGATGTGCAAGATCAGTGGATTGGTCCA 242

Qy        405 TTCGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCT 464
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Qy        465 GCATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATT 524
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Qy        525 TCTTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGT 584
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Qy        585 CGATGGAAGCTTTTAC 600
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RESULT 11
US-11-060-756-6763
; Sequence 6763, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6763
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-6763

Query Match 5.2%; Score 61.6; DB 10; Length 1400;
Best Local Similarity 46.3%; Pred. No. 1.6e-07;
Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

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Qy        345 CGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAA 404
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Qy        405 TTCGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCT 464
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Qy        465 GCATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATT 524
Db        303 GTGTGTGGTCTACCCTTTTAAACCAAAGCTCACTATCAAGACAGCGTTTGTCATTATTAT 362

Qy        525 TCTTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGT 584
Db        363 GATCATCTGGGTCCTAGCCATCACCATTATGTCTCCATCTGCAGTAATGTTACATGTGCA 422

Qy        585 CGATGGAAGCTTTTAC 600
Db        423 AGAAGAAAAATATTAC 438
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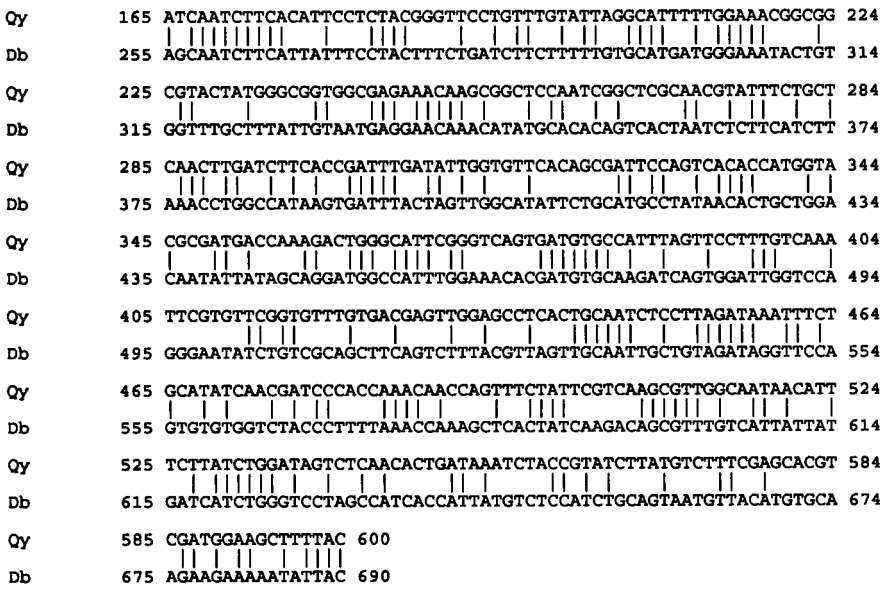
RESULT 12
US-10-060-369-8
; Sequence 8, Application US/10060369
; Publication No. US20030139589A1
; GENERAL INFORMATION:
; APPLICANT: Zastawny, Roman
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR A4
; FILE REFERENCE: 2931-104
; CURRENT APPLICATION NUMBER: US/10/060,369
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 09/173565
; PRIOR FILING DATE: 1998-08-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 1440
; TYPE: DNA
; ORGANISM: Human
US-10-060-369-8

Query Match 5.2%; Score 61.6; DB 6; Length 1440;
Best Local Similarity 46.3%; Pred. No. 1.6e-07;
Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;



RESULT 13
US-10-507-617-4
; Sequence 4, Application US/10507617
; Publication No. US20050119206A1
; GENERAL INFORMATION:
; APPLICANT: Eulenberg, Karsten
; APPLICANT: Steuernagel, Arnd
; APPLICANT: Haeder, Thomas
; APPLICANT: Broenner, Guenter
; TITLE OF INVENTION: CG8327, CG10823, CG18418, CG15862, CG3768, CG11447 and CG16750
; TITLE OF INVENTION: Homologous Proteins Involved in the Regulation of Energy
; TITLE OF INVENTION: Homeostasis
; FILE REFERENCE: 2923-651
; CURRENT APPLICATION NUMBER: US/10/507,617
; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: PCT/EP03/02714
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: EP 02 005 882.2
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: EP 002 006 012.5
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: EP 02 006 271.7
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: EP 02 006 810.2
; PRIOR FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-507-617-4

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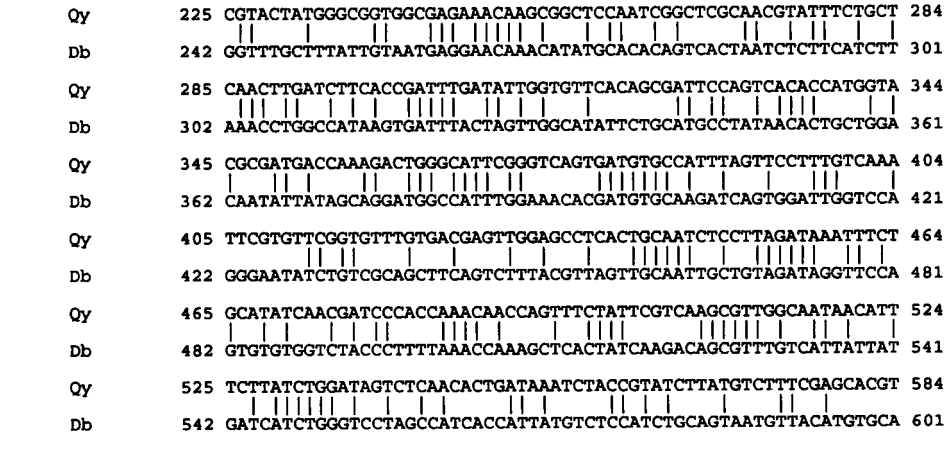
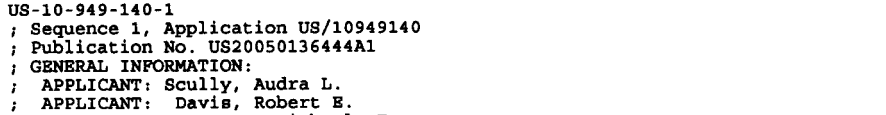
Best Local Similarity 46.3%; Pred. No. 1.7e-07;
Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;



RESULT 14
US-10-949-140-1
; Sequence 1, Application US/10949140
; Publication No. US20050136444A1
; GENERAL INFORMATION:
; APPLICANT: Scully, Audra L.
; APPLICANT: Davis, Robert E.
; APPLICANT: Vanover, Kimberly E.
; APPLICANT: Gardell, Luis Roberto
; APPLICANT: Lameh, Jelveh
; APPLICANT: Kelly, Nicholas Michael
; APPLICANT: Bertozzi, Fabio
; TITLE OF INVENTION: TREATING NEUROPATHIC PAIN WITH
; TITLE OF INVENTION: NEUROPEPTIDE FF RECEPTOR 2 AGONISTS
; FILE REFERENCE: ACADIA.038A
; CURRENT APPLICATION NUMBER: US/10/949,140
; CURRENT FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: 60/508,008
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: 60/506,130
; PRIOR FILING DATE: 2003-09-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-949-140-1

Query Match 5.2%; Score 61.6; DB 9; Length 1560;
Best Local Similarity 46.3%; Pred. No. 1.7e-07;
Matches 202; Conservative 0; Mismatches 234; Indels 0; Gaps 0;



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Qy        585 CGATGGAAGCTTTTAC 600

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RESULT 15
US-10-276-774-743
; Sequence 743, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  APPLICANT:  Tang, Y, Tom et al
;  TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
;  FILE REFERENCE: 21272-030
;  CURRENT APPLICATION NUMBER: US/10/276,774
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 09/560,875
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 09/496,914
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 2700
;  SOFTWARE: Custom
; SEQ ID NO 743
;   LENGTH: 1824
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-276-774-743

  Query Match             5.2%;  Score 61.6;  DB 7;  Length 1824;
  Best Local Similarity   46.3%;  Pred. No. 1.9e-07;
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4	57.8	4.8	1605	18	US-11-183-615-3	Sequence 3, Appli
5	57.8	4.8	1888	17	US-11-080-991-25	Sequence 25, Appl
6	57.8	4.8	2752	13	US-10-960-414-9	Sequence 9, Appli
7	53.4	4.5	1329	18	US-11-100-640-33	Sequence 33, Appl
8	53.4	4.5	1578	9	US-10-473-173-20	Sequence 20, Appl
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17	47.4	4.0	1334	10	US-10-992-577-43	Sequence 43, Appl
18	47.4	4.0	2471	17	US-11-136-527-2231	Sequence 2231, Ap
19	47.2	4.0	1450	17	US-11-136-527-3841	Sequence 3841, Ap
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21	47	3.9	1560	17	US-11-136-527-3742	Sequence 3742, Ap
22	47	3.9	1865	10	US-10-533-355-9	Sequence 9, Appli
23	46.6	3.9	1069	18	US-11-183-615-5	Sequence 5, Appli
24	46.6	3.9	1201	18	US-11-183-615-16	Sequence 16, Appl
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30	45.4	3.8	1452	17	US-11-136-527-3122	Sequence 3122, Ap
31	45.2	3.8	1290	17	US-11-136-527-2457	Sequence 2457, Ap
32	45.2	3.8	1290	17	US-11-136-527-6553	Sequence 6553, Ap
33	45	3.8	3288	17	US-11-136-527-3178	Sequence 3178, Ap
34	44.8	3.8	1290	18	US-11-223-294-56	Sequence 56, Appl
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36	44.2	3.7	1677	18	US-11-262-284-33	Sequence 33, Appl
37	44	3.7	1339	17	US-11-136-527-4061	Sequence 4061, Ap
38	44	3.7	1339	18	US-11-224-663-596	Sequence 596, App
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40	44	3.7	2580	17	US-11-136-527-3525	Sequence 3525, Ap
41	43.4	3.6	1504	17	US-11-136-527-3501	Sequence 3501, Ap
42	43.4	3.6	2422	17	US-11-136-527-2272	Sequence 2272, Ap
43	43.2	3.6	1290	18	US-11-223-294-55	Sequence 55, Appl
44	43.2	3.6	1293	10	US-10-992-577-7	Sequence 7, Appli
45	43.2	3.6	1293	11	US-10-508-892-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-11-136-527-2424
; Sequence 2424, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2424
; LENGTH: 2025
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2424

Query Match 5.2%; Score 62.2; DB 17; Length 2025;
Best Local Similarity 50.5%; Pred. No. 5e-07;
Matches 151; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

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Qy      165 ATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGG 224
            ||  |||  |||  |  | |   |  || |||| ||  ||||||| | || |||  |
Db      554 ATACATCAACACGATTGTATCATGCCTCGTGTTCGTGCTAGGCATCATCGGGAACTCCAC 613

Qy      225 CGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT 284
              | |||  |      |    | ||||| |  |   |   | || |||  | ||  |
Db      614 ACTGCTAAGAATCATCTACAAGAACAAGTGCATGAGAAATGGTCCCAATATCTTGATCGC 673

Qy      285 CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTA 344
            ||  ||    |   ||| || ||    |  |||  |  ||||  | |  | |  |
Db      674 CAGCCTGGCTCTGGGAGATCTGCTACACATCATCATCGACATTCCCATTAATGCCTACAA 733
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Qy        345 CGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAA 404
              |  |||  |     |||||| ||||  ||  |  |  |||||||  |   |  ||  ||  ||     |  ||
Db        734 GCTGCTGGCAGGGGACTGGCCATTTGGAGCTGAGATGTGCAAGCTGGTGCCSTTCATACA 793

Qy        405 TTCGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTC 463
                |  |||  |||     | ||     | |||  ||    |||   |       |  ||  |  ||  ||
Db        794 GAAGGCTTCTGTGGGGATCACAGTGTTGAGTCTATGTGCTCTAAGTATTGACAGATATC 852


RESULT 2
US-10-992-577-5
; Sequence 5, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
;  APPLICANT: Gerald, Christophe P.G.
;  APPLICANT:  Jones, Kenneth A.
;  APPLICANT:  Bonini, James A.
;  APPLICANT:  Borowsky, Beth E.
;  APPLICANT:  Craig, Douglas A.
;  TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
;  TITLE OF INVENTION:  And Uses Thereof
;  FILE REFERENCE: 57155-D/JPW
;  CURRENT APPLICATION NUMBER: US/10/992,577
;  CURRENT FILING DATE:  2004-11-18
;  PRIOR APPLICATION NUMBER: US/09/538,036
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: 09/405,558
;  PRIOR FILING DATE: 1999-09-24
;  PRIOR APPLICATION NUMBER: 09/255,368
;  PRIOR FILING DATE: 1999-02-22
;  PRIOR APPLICATION NUMBER: 09/161,113
;  PRIOR FILING DATE: 1998-09-25
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 1302
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-992-577-5

  Query Match             5.2%;  Score 61.6;  DB 10;  Length 1302;
  Best Local Similarity   46.3%;  Pred. No. 6.4e-07;
  Matches  202;  Conservative    0;  Mismatches  234;  Indels    0;  Gaps    0;

Qy        165 ATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGG 224
              | |||||||||    |    ||||     |  | ||  | ||  ||||  | |||||     |
Db        165 AGCAATCTTCATTATTTCCTACTTTCTGATCTTCTTTTTGTGCATGATGGGAAATACTGT 224

Qy        225 CGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT 284
              ||     |     ||   ||| |||||  |    | ||  | |      ||  | ||  |  |
Db        225 GGTTTGCTTTATTGTAATGAGGAACAAACATATGCACACAGTCACTAATCTCTTCATCTT 284

Qy        285 CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTA 344
              |||  ||  | | |  |||||  ||  | |    |      ||  ||  | ||||    | |
Db        285 AAACCTGGCCATAAGTGATTTACTAGTTGGCATATTCTGCATGCCTATAACACTGCTGGA 344

Qy        345 CGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAA 404
              |   ||  |    ||  |||  ||||  ||       |||||||  |   |    |  |||    |
Db        345 CAATATTATAGCAGGATGGCCATTTGGAAACACGATGTGCAAGATCAGTGGATTGGTCCA 404

Qy        405 TTCGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCT 464
                 ||  ||     |    |   |    |  |    ||||||  |  ||||||  ||  |
Db        405 GGGAATATCTGTCGCAGCTTCAGTCTTTACGTTAGTTGCAATTGCTGTAGATAGGTTCCA 464

Qy        465 GCATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATT 524
              |  |  |   | |  ||    ||||  |    |  ||||      ||||||  |  ||  |  |
Db        465 GTGTGTGGTCTACCCTTTTAAACCAAAGCTCACTATCAAGACAGCGTTTGTCATTATTAT 524

Qy        525 TCTTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGT 584
                |||||||  |   |  |  |     ||  |     ||  |  |     |    ||  |
Db        525 GATCATCTGGGTCCTAGCCATCACCATTATGTCTCCATCTGCAGTAATGTTACATGTGCA 584

Qy        585 CGATGGAAGCTTTTAC 600
                 || |  ||  | ||||
Db        585 AGAAGAAAAATATTAC 600


RESULT 3
US-10-510-018-1
; Sequence 1, Application US/10510018
; Publication No. US20050244896A1
; GENERAL INFORMATION:
;  APPLICANT: Golz, Stefan
;  APPLICANT:  Bruggemeier, Ulf
;  APPLICANT:  Weingarten, Bernhard
;  TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
;  TITLE OF INVENTION:  Neuropeptide FF Receptor 2 (NPFF2)
;  FILE REFERENCE: Le A 35 945
;  CURRENT APPLICATION NUMBER: US/10/510,018
;  CURRENT FILING DATE:  2004-10-01
;  PRIOR APPLICATION NUMBER: PCT/EP2003/002962
;  PRIOR FILING DATE: 2003-03-21
;  PRIOR APPLICATION NUMBER: EP 02007270.8
;  PRIOR FILING DATE: 2002-04-02
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
;   LENGTH: 1936
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-510-018-1

  Query Match             5.2%;  Score 61.6;  DB 10;  Length 1936;
  Best Local Similarity   46.3%;  Pred. No. 7.3e-07;
  Matches  202;  Conservative    0;  Mismatches  234;  Indels    0;  Gaps    0;

Qy        165 ATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGG 224
              | |||||||||    |    ||||     |  | ||  | ||  ||||  | |||||     |
Db        539 AGCAATCTTCATTATTTCCTACTTTCTGATCTTCTTTTTGTGCATGATGGGAAATACTGT 598

Qy        225 CGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT 284
              ||     |     ||   ||| |||||  |    | ||  | |      ||  | ||  |  |
Db        599 GGTTTGCTTTATTGTAATGAGGAACAAACATATGCACACAGTCACTAATCTCTTCATCTT 658

Qy        285 CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTA 344
              |||  ||  | | |  |||||  ||  | |    |      ||  ||  | ||||    | |
Db        659 AAACCTGGCCATAAGTGATTTACTAGTTGGCATATTCTGCATGCCTATAACACTGCTGGA 718

Qy        345 CGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAA 404
              |   ||  |    ||  |||  ||||  ||       |||||||  |   |    |  |||    |
Db        719 CAATATTATAGCAGGATGGCCATTTGGAAACACGATGTGCAAGATCAGTGGATTGGTCCA 778

Qy        405 TTCGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCT 464
                 ||  ||     |    |   |    |  |    ||||||  |  ||||||  ||  |
Db        779 GGGAATATCTGTCGCAGCTTCAGTCTTTACGTTAGTTGCAATTGCTGTAGATAGGTTCCA 838

Qy        465 GCATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATT 524
              |  |  |   | |  ||    ||||  |    |  ||||      ||||||  |  ||  |  |
Db        839 GTGTGTGGTCTACCCTTTTAAACCAAAGCTCACTATCAAGACAGCGTTTGTCATTATTAT 898

Qy        525 TCTTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGT 584
                |||||||  |   |  |  |     ||  |     ||  |  |     |    ||  |
Db        899 GATCATCTGGGTCCTAGCCATCACCATTATGTCTCCATCTGCAGTAATGTTACATGTGCA 958

Qy        585 CGATGGAAGCTTTTAC 600
                 || |  ||  | ||||
Db        959 AGAAGAAAAATATTAC 974


RESULT 4
US-11-183-615-3
; Sequence 3, Application US/11183615
; Publication No. US20060040964A1
; GENERAL INFORMATION:
;  APPLICANT: Bakthavatchalam, Rajagopal
;  APPLICANT:  Blum, Charles  A.
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;  APPLICANT:  Brielmann, Harry L.
;  APPLICANT:  Darrow, James W.
;  APPLICANT:  De Lombaert, Stephane W.
;  APPLICANT:  Hutchinson, Alan W.
;  APPLICANT:  Tran, Jennifer W.
;  APPLICANT:  Zheng, Xiaozhang W.
;  APPLICANT:  Elliott, Richard  L.
;  APPLICANT:  Hammond, Marlys L.
;  TITLE OF INVENTION: SPIRO[ISOBENZOFURAN-1,4'-PIPERIDIN]-3-ONES AND
;  TITLE OF INVENTION:  3H-SPIROISOBENZOFURAN-1,4'-PIPERIDINES
;  FILE REFERENCE: U 014539-7
;  CURRENT APPLICATION NUMBER: US/11/183,615
;  CURRENT FILING DATE:  2005-07-18
;  PRIOR APPLICATION NUMBER: US/10/410,648
;  PRIOR FILING DATE: 2003-04-09
;  PRIOR APPLICATION NUMBER: 10/013,846
;  PRIOR FILING DATE: 2001-12-11
;  PRIOR APPLICATION NUMBER: 60/254,990
;  PRIOR FILING DATE: 2000-12-12
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 1605
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-183-615-3

  Query Match             4.8%;  Score 57.8;  DB 18;  Length 1605;
  Best Local Similarity   46.4%;  Pred. No. 8.4e-06;
  Matches  188;  Conservative    0;  Mismatches  217;  Indels    0;  Gaps    0;

Qy         75 AAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATTGCGGCACAAGGCAT 134
              || ||||||   | |       | |    |||    ||    | ||  |||    | |
Db        226 AAATCATTCAGTCCACTCTAATTTCTCAGAGAAGAATGCCCAGCTTCTGGCTTTTGAAAA 285

Qy        135 CGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCCT 194
              ||||||  |  | |   |||  |||   ||  | |||  |  |    || ||     |
Db        286 TGATGATTGTCATCTGCCCTTGGCCATGATATTTACCTTAGCTCTTGCTTATGGAGCTGT 345

Qy        195 GTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAAACAAGCG 254
              | |  |  | ||  | | |||||||   | | |  |        |   || | | |||
Db        346 GATCATTCTTGGTGTCTCTGGAAACCTGGCCTTGATCATAATCATCTTGAAACAAAAGGA 405

Qy        255 GCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATATTGGT 314
              | |   |  | |  |||| |  |  |  | ||| |   |||| | || ||| |  | |
Db        406 GATGAGAAATGTTACCAACATCCTGATTGTGAACCTTTCCTTCTCAGACTTGCTTGTTGC 465

Qy        315 GTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGACTGGGCATTCGGGTC 374
                |||      | ||  | |||      ||| |  | |   |  ||||||  || ||
Db        466 CATCATGTGTCTCCCCTTTACATTTGTCTACACATTAATGGACCACTGGGTCTTTGGTGA 525

Qy        375 AGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTTGTGACGAGTTGGAG 434
              | |||||||  | ||   ||||||      | |    |||  |   |||| | | ||
Db        526 GGCGATGTGTAAGTTGAATCCTTTTGTGCAATGTGTTTCAATCACTGTGTCCATTTTCTC 585

Qy        435 CCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCC 479
              ||    |  ||  | | ||   |  || ||  || | | | ||
Db        586 TCTGGTTCTCATTGCTGTGGAACGACATCAGCTGATAATCAACCC 630


RESULT 5
US-11-080-991-25
; Sequence 25, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
;  APPLICANT: Veiby, Petter Ole
;  TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
;  TITLE OF INVENTION:  AND OVARIAN CANCER
;  FILE REFERENCE: MRI-039
;  CURRENT APPLICATION NUMBER: US/11/080,991
;  CURRENT FILING DATE:  2005-03-11
;  PRIOR APPLICATION NUMBER: US/10/176,847
;  PRIOR FILING DATE: 2002-06-21
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 1888
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1814, 1834, 1850
;   OTHER INFORMATION: n = A,T,C or G
US-11-080-991-25

  Query Match             4.8%;  Score 57.8;  DB 17;  Length 1888;
  Best Local Similarity   46.4%;  Pred. No. 8.9e-06;
  Matches  188;  Conservative    0;  Mismatches  217;  Indels    0;  Gaps    0;

Qy         75 AAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATTGCGGCACAAGGCAT 134
              || ||||||   | |       | |    |||    ||    | ||  |||    | |
Db        498 AAATCATTCAGTCCACTCTAATTTCTCAGAGAAGAATGCCCAGCTTCTGGCTTTTGAAAA 557

Qy        135 CGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCCT 194
              ||||||  |  | |   |||  |||   ||  | |||  |  |    || ||     |
Db        558 TGATGATTGTCATCTGCCCTTGGCCATGATATTTACCTTAGCTCTTGCTTATGGAGCTGT 617

Qy        195 GTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAAACAAGCG 254
              | |  |  | ||  | | |||||||   | | |  |        |   || | | |||
Db        618 GATCATTCTTGGTGTCTCTGGAAACCTGGCCTTGATCATAATCATCTTGAAACAAAAGGA 677

Qy        255 GCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATATTGGT 314
              | |   |  | |  |||| |  |  |  | ||| |   |||| | || ||| |  | |
Db        678 GATGAGAAATGTTACCAACATCCTGATTGTGAACCTTTCCTTCTCAGACTTGCTTGTTGC 737

Qy        315 GTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGACTGGGCATTCGGGTC 374
                |||      | ||  | |||      ||| |  | |   |  ||||||  || ||
Db        738 CATCATGTGTCTCCCCTTTACATTTGTCTACACATTAATGGACCACTGGGTCTTTGGTGA 797

Qy        375 AGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTTGTGACGAGTTGGAG 434
              | |||||||  | ||   ||||||      | |    |||  |   |||| | | ||
Db        798 GGCGATGTGTAAGTTGAATCCTTTTGTGCAATGTGTTTCAATCACTGTGTCCATTTTCTC 857

Qy        435 CCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCC 479
              ||    |  ||  | | ||   |  || ||  || | | | ||
Db        858 TCTGGTTCTCATTGCTGTGGAACGACATCAGCTGATAATCAACCC 902


RESULT 6
US-10-960-414-9
; Sequence 9, Application US/10960414
; Publication No. US20060074565A1
; GENERAL INFORMATION:
;  APPLICANT: MILLER, LANCE D.
;  APPLICANT:  GEORGE, JOSHY
;  APPLICANT:  VEGA, VINSENSIUS B.
;  TITLE OF INVENTION: METHODS, SYSTEMS, AND COMPOSITIONS FOR CLASSIFICATION,
;  TITLE OF INVENTION:  PROGNOSIS, AND DIAGNOSIS OF CANCERS
;  FILE REFERENCE: 38271-76067
;  CURRENT APPLICATION NUMBER: US/10/960,414
;  CURRENT FILING DATE:  2004-10-06
;  NUMBER OF SEQ ID NOS: 500
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
;   LENGTH: 2752
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-960-414-9

  Query Match             4.8%;  Score 57.8;  DB 13;  Length 2752;
  Best Local Similarity   46.4%;  Pred. No. 1e-05;
  Matches  188;  Conservative    0;  Mismatches  217;  Indels    0;  Gaps    0;

Qy         75 AAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATTGCGGCACAAGGCAT 134
              || ||||||   | |       | |    |||    ||    | ||  |||    | |
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Db        238 AAATCATTCAGTCCACTCTAATTTCTCAGAGAAGAATGCCCAGCTTCTGGCTTTTGAAAA 297

Qy        135 CGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCCT 194
              ||||||  |  | |   |||   |||   ||  | |||  |  |     || ||      |
Db        298 TGATGATTGTCATCTGCCCTTGGCCATGATATTTACCTTAGCTCTTGCTTATGGAGCTGT 357

Qy        195 GTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAAACAAGCG 254
              | |  |  | ||  | | |||||||  | | |  |      |   || | | |||
Db        358 GATCATTCTTGGTGTCTCTGGAAACCTGGCCTTGATCATAATCATCTTGAAACAAAAGGA 417

Qy        255 GCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATATTGGT 314
              | |   |   | |  |||| |  |  |  | ||| |   |||| | || ||| |  | |
Db        418 GATGAGAAATGTTACCAACATCCTGATTGTGAACCTTTCCTTCTCAGACTTGCTTGTTGC 477

Qy        315 GTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGACTGGGCATTCGGGTC 374
              |||       | ||  | |||      ||| |  | |   | ||||||  || ||
Db        478 CATCATGTGTCTCCCCTTTACATTTGTCTACACATTAATGGACCACTGGGTCTTTGGTGA 537

Qy        375 AGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTTGTGACGAGTTGGAG 434
              | ||||||  | ||   ||||||     | |    |||  |   |||| | | ||
Db        538 GGCGATGTGTAAGTTGAATCCTTTTGTGCAATGTGTTTCAATCACTGTGTCCATTTTCTC 597

Qy        435 CCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCC 479
              ||    |   ||  |  | ||   |  || ||  || | | | ||
Db        598 TCTGGTTCTCATTGCTGTGGAACGACATCAGCTGATAATCAACCC 642
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RESULT 7
US-11-100-640-33
; Sequence 33, Application US/11100640
; Publication No. US20060035244A1
; GENERAL INFORMATION:
;  APPLICANT: Riggins, Gregory J
;  TITLE OF INVENTION: A Method for Distinguishing Follicular Tyroid Adenoma (FTA) from
;  TITLE OF INVENTION:  Follicular Thyroid Carcinoma (PTC)
;  FILE REFERENCE: 000250.00021
;  CURRENT APPLICATION NUMBER: US/11/100,640
;  CURRENT FILING DATE:  2005-04-07
;  NUMBER OF SEQ ID NOS: 98
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
;   LENGTH: 1329
;   TYPE: DNA
;   ORGANISM: human
US-11-100-640-33

  Query Match             4.5%;  Score 53.4;  DB 18;  Length 1329;
  Best Local Similarity   48.5%;  Pred. No. 0.00014;
  Matches  147;  Conservative    0;  Mismatches  156;  Indels    0;  Gaps    0;

Qy        161 TCCGATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACG 220
              ||  ||  |||  |||  |  | | | |  |  |||| ||  | || ||  | || |||
Db        299 TCAAATACATCAACACGGTTGTGTCCTGCCTTGTGTTCGTGCTGGGGATCATCGGGAACT 358

Qy        221 GCGGCGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTC 280
              |   | ||  |   |   |  ||||||  |  | | |   |  || |||  | ||
Db        359 CCACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGA 418

Qy        281 TGCTCAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCAT 340
              |   || ||||     |     ||  || |     | |||  |  || ||  |||     |
Db        419 TCGCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCT 478

Qy        341 GGTACGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGT 400
              |    | ||  |  | |||||| |||| ||  | | ||||||  |  | || |||||
Db        479 ACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCA 538

Qy        401 CAAATTCGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAAT 460
              | |     || |||    | ||     ||| ||   |||  |     | || | ||
Db        539 TACAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGAT 598

Qy        461 TTC 463
              |||
Db        599 ATC 601
```

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RESULT 8
US-10-473-173-20
; Sequence 20, Application US/10473173
; Publication No. US20060088823A1
; GENERAL INFORMATION:
;  APPLICANT: VAN ANDEL INSTITUTE
;  TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
;  TITLE OF INVENTION:  Carcinoma: Prognosis and Drug Target Identification
;  FILE REFERENCE: 38345-170094
;  CURRENT APPLICATION NUMBER: US/10/473,173
;  CURRENT FILING DATE:  2003-09-29
;  PRIOR APPLICATION NUMBER: US 60/279,411
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 498
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;   LENGTH: 1578
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-473-173-20

  Query Match             4.5%;  Score 53.4;  DB 9;  Length 1578;
  Best Local Similarity   48.5%;  Pred. No. 0.00015;
  Matches  147;  Conservative    0;  Mismatches  156;  Indels    0;  Gaps    0;

Qy        161 TCCGATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACG 220
              ||  ||  |||  |||  |  | | | |  |  |||| ||  | || ||  | || |||
Db        532 TCAAATACATCAACACGGTTGTGTCCTGCCTTGTGTTCGTGCTGGGGATCATCGGGAACT 591

Qy        221 GCGGCGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTC 280
              |   | ||  |   |   |  ||||||  |  | | |   |  || |||  | ||
Db        592 CCACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGA 651

Qy        281 TGCTCAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCAT 340
              |   || ||||     |     ||  || |     | |||  |  || ||  |||     |
Db        652 TCGCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCT 711

Qy        341 GGTACGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGT 400
              |    | ||  |  | |||||| |||| ||  | | ||||||  |  | || |||||
Db        712 ACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCA 771

Qy        401 CAAATTCGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAAT 460
              | |     || |||    | ||     ||| ||   |||  |     | || | ||
Db        772 TACAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGAT 831

Qy        461 TTC 463
              |||
Db        832 ATC 834
```

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RESULT 9
US-11-223-294-38
; Sequence 38, Application US/11223294
; Publication No. US20060035332A1
; GENERAL INFORMATION:
;  APPLICANT: HINUMA, Shuji
;  APPLICANT:  YOSHIDA, Hiromi
;  APPLICANT:  HABATA, Yugo
;  APPLICANT:  HOSOYA, Masaki
;  APPLICANT:  KITADA, Chieko
;  TITLE OF INVENTION: Novel RFRP-3 And Its DNA
;  FILE REFERENCE: 2944US0P
;  CURRENT APPLICATION NUMBER: US/11/223,294
;  CURRENT FILING DATE:  2005-09-09
;  PRIOR APPLICATION NUMBER: US/10/487,634
;  PRIOR FILING DATE: 2004-02-24
;  PRIOR APPLICATION NUMBER: PCT/JP02/08466
;  PRIOR FILING DATE: 2002-08-22
;  PRIOR APPLICATION NUMBER: JP 2001-254826
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 78
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; SEQ ID NO 38
; LENGTH: 1299
; TYPE: DNA
; ORGANISM: Rat
US-11-223-294-38

Query Match 4.2%; Score 50; DB 18; Length 1299;
Best Local Similarity 45.9%; Pred. No. 0.0013;
Matches 170; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

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Qy        165 ATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGG 224
              | | || ||||         |||||  | || | ||  |  |  ||||  | || |||  |
Db        129 AGCCATGTTCATCGCGGCCTACGTGCTCATCTTCCTCCTCTGCATGGTGGGCAACACCCT 188

Qy        225 CGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT 284
              ||    |     |||    |  |||  ||   | |   | |    ||||  | |||  | ||
Db        189 GGTCTGCTTCATTGTGCTCAAGAACCGGCACATGCGCACTGTCACCAACATGTTTATCCT 248

Qy        285 CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTA 344
              ||||  ||  | |||  |||   ||  |  |||    ||        || ||    ||  |   | |
Db        249 CAACCTGGCCGTCAGCGACCTGCTGGTGGGCATCTTCTGCATGCCCACAACCCTTGTGGA 308

Qy        345 CGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAA 404
              |    | | ||  |  |||  | ||  |     |  |  |||  |  |        |||    |
Db        309 CAACCTTATCACTGGTTGGCCTTTTGACAACGCCACATGCAAGATGAGCGGCTTGGTGCA 368

Qy        405 TTCGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCT 464
                  || |||| ||   ||  ||  |  ||    || ||| |  | || |  || |
Db        369 GGGCATGTCCGTGTCTGCATCGGTTTTCACACTGGTGGCCATCGCTGTGGAAAGGTTCCG 428

Qy        465 GCATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATT 524
                |||    | ||   |      |     |  |  ||||  | ||| ||   |  |
Db        429 CTGCATCGTGCACCCTTTCCGCGAGAAGCTGACCCTTCGGAAGGCGCTGTTCACCATCGC 488

Qy        525 TCTTATCTGG 534
                | ||||||
Db        489 GGTGATCTGG 498
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RESULT 10
US-10-992-577-1
; Sequence 1, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; TITLE OF INVENTION: And Uses Thereof
; FILE REFERENCE: 57155-D/JPW
; CURRENT APPLICATION NUMBER: US/10/992,577
; CURRENT FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: US/09/538,036
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/405,558
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 09/255,368
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1410
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-992-577-1

Query Match 4.2%; Score 50; DB 10; Length 1410;
Best Local Similarity 45.9%; Pred. No. 0.0014;
Matches 170; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

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Qy        165 ATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGG 224
              | | || ||||         |||||  | || | ||  |  |  ||||  | || |||  |
Db        201 AGCCATGTTCATCGCGGCCTACGTGCTCATCTTCCTCCTCTGCATGGTGGGCAACACCCT 260

Qy        225 CGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT 284
              ||    |     |||    |  |||  ||   | |   | |    ||||  | |||  | ||
Db        261 GGTCTGCTTCATTGTGCTCAAGAACCGGCACATGCGCACTGTCACCAACATGTTTATCCT 320

Qy        285 CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTA 344
              ||||  ||  | |||  |||   ||  |  |||    ||        || ||    ||  |   | |
Db        321 CAACCTGGCCGTCAGCGACCTGCTGGTGGGCATCTTCTGCATGCCCACAACCCTTGTGGA 380

Qy        345 CGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAA 404
              |    | | ||  |  |||  | ||  |     |  |  |||  |  |        |||    |
Db        381 CAACCTTATCACTGGTTGGCCTTTTGACAACGCCACATGCAAGATGAGCGGCTTGGTGCA 440

Qy        405 TTCGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCT 464
                  || |||| ||   ||  ||  |  ||    || ||| |  | || |  || |
Db        441 GGGCATGTCCGTGTCTGCATCGGTTTTCACACTGGTGGCCATCGCTGTGGAAAGGTTCCG 500

Qy        465 GCATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATT 524
                |||    | ||   |      |     |  |  ||||  | ||| ||   |  |
Db        501 CTGCATCGTGCACCCTTTCCGCGAGAAGCTGACCCTTCGGAAGGCGCTGTTCACCATCGC 560

Qy        525 TCTTATCTGG 534
                | ||||||
Db        561 GGTGATCTGG 570
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RESULT 11
US-11-136-527-4059
; Sequence 4059, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4059
; LENGTH: 3219
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-4059

Query Match 4.1%; Score 48.8; DB 17; Length 3219;
Best Local Similarity 51.4%; Pred. No. 0.004;
Matches 113; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

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Qy        152 ACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTT 211
              ||  ||||||        ||  || |  |||||||  |  ||  | |||||  | || || |
Db        342 ACAGTTACATATTTGTCATGATCCCTACCCTCTACAGCATCATCTTTGTGGTGGGAATAT 401

Qy        212 TTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCA 271
              ||||||||  ||   ||  |    |   |          ||| |  |||  |  | |    ||
Db        402 TTGGAAACAGCTTGGTGGTGATTGTCATTTACTTTTACATGAAGCTGAAGACTGTGGCCA 461

Qy        272 ACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAG 331
              |||  |||||  |||||  |   |||  | || ||    ||  || | ||   |   |
Db        462 GCGTCTTTCTTCTCAATCTCGCCTTGGCTGACTTATGCTTTTTGCTGACTTTGCCCCTGT 521

Qy        332 TCACACCATGGTACGCGATGACCAAAGACTGGGCATTCGG 371
              ||   |    |||  |||     |   ||||  | |||||
Db        522 GGGCAGTCTATACCGCTATGGAGTACCGCTGGCCCTTCGG 561
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RESULT 12

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US-11-224-663-594
; Sequence 594, Application US/11224663
; Publication No. US20060078921A1
; GENERAL INFORMATION:
;  APPLICANT: BOESS, FRANZISKA
;  APPLICANT:  SUTER-DICK, LAURA
;  APPLICANT:  WOLF, DETLEF
;  TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
;  FILE REFERENCE: 21199 US2
;  CURRENT APPLICATION NUMBER: US/11/224,663
;  CURRENT FILING DATE:  2005-09-12
;  PRIOR APPLICATION NUMBER: 10/388,934
;  PRIOR FILING DATE: 2003-03-14
;  PRIOR APPLICATION NUMBER: EP 02005336.9
;  PRIOR FILING DATE: 2002-03-14
;  PRIOR APPLICATION NUMBER: EP 02015657.6
;  PRIOR FILING DATE: 2002-07-17
;  NUMBER OF SEQ ID NOS: 862
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 594
;   LENGTH: 3219
;   TYPE: DNA
;   ORGANISM: Rattus rattus
US-11-224-663-594

  Query Match             4.1%;  Score 48.8;  DB 18;  Length 3219;
  Best Local Similarity   51.4%;  Pred. No. 0.004;
  Matches  113;  Conservative    0;  Mismatches  107;  Indels    0;  Gaps    0;

Qy        152 ACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTT 211
              ||  ||||||        ||  || |  |||||||  |  || | |||||  | || || |
Db        342 ACAGTTACATATTTGTCATGATCCCTACCCTCTACAGCATCATCTTTGTGGTGGGAATAT 401

Qy        212 TTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCA 271
              ||||||||  ||   ||  |   |   |        |||  |  |||  |  | |   ||
Db        402 TTGGAAACAGCTTGGTGGTGATTGTCATTTACTTTTACATGAAGCTGAAGACTGTGGCCA 461

Qy        272 ACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAG 331
              |||  |||||  |||||  |   |||  | ||  ||    ||  || |  |   |
Db        462 GCGTCTTTCTTCTCAATCTCGCCTTGGCTGACTTATGCTTTTTGCTGACTTTGCCCCTGT 521

Qy        332 TCACACCATGGTACGCGATGACCAAAGACTGGGCATTCGG 371
                ||   |   |||  |||    |   ||||  | |||||
Db        522 GGGCAGTCTATACCGCTATGGAGTACCGCTGGCCCTTCGG 561


RESULT 13
US-11-224-525-594
; Sequence 594, Application US/11224525
; Publication No. US20060084096A1
; GENERAL INFORMATION:
;  APPLICANT: BOESS, FRANZISKA
;  APPLICANT:  SUTER-DICK, LAURA
;  APPLICANT:  WOLF, DETLEF
;  TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
;  FILE REFERENCE: 21199 US1
;  CURRENT APPLICATION NUMBER: US/11/224,525
;  CURRENT FILING DATE:  2005-09-12
;  PRIOR APPLICATION NUMBER: 10/388,934
;  PRIOR FILING DATE: 2003-03-14
;  PRIOR APPLICATION NUMBER: EP 02005336.9
;  PRIOR FILING DATE: 2002-03-14
;  PRIOR APPLICATION NUMBER: EP 02015657.6
;  PRIOR FILING DATE: 2002-07-17
;  NUMBER OF SEQ ID NOS: 862
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 594
;   LENGTH: 3219
;   TYPE: DNA
;   ORGANISM: Rattus rattus
US-11-224-525-594

  Query Match             4.1%;  Score 48.8;  DB 18;  Length 3219;
  Best Local Similarity   51.4%;  Pred. No. 0.004;
  Matches  113;  Conservative    0;  Mismatches  107;  Indels    0;  Gaps    0;

Qy        152 ACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTT 211
              ||  ||||||        ||  || |  |||||||  |  || | |||||  | || || |
Db        342 ACAGTTACATATTTGTCATGATCCCTACCCTCTACAGCATCATCTTTGTGGTGGGAATAT 401

Qy        212 TTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCA 271
              ||||||||  ||   ||  |   |   |        |||  |  |||  |  | |   ||
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Qy        272 ACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAG 331
              |||  |||||  |||||  |   |||  | ||  ||    ||  || |  |   |
Db        462 GCGTCTTTCTTCTCAATCTCGCCTTGGCTGACTTATGCTTTTTGCTGACTTTGCCCCTGT 521

Qy        332 TCACACCATGGTACGCGATGACCAAAGACTGGGCATTCGG 371
                ||   |   |||  |||    |   ||||  | |||||
Db        522 GGGCAGTCTATACCGCTATGGAGTACCGCTGGCCCTTCGG 561


RESULT 14
US-11-136-527-3736
; Sequence 3736, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: US 60/574,294
;  PRIOR FILING DATE: 2005-05-26
;  NUMBER OF SEQ ID NOS: 362830
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3736
;   LENGTH: 3295
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-11-136-527-3736

  Query Match             4.1%;  Score 48.8;  DB 17;  Length 3295;
  Best Local Similarity   51.4%;  Pred. No. 0.004;
  Matches  113;  Conservative    0;  Mismatches  107;  Indels    0;  Gaps    0;

Qy        152 ACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTT 211
              ||  ||||||        ||  || |  |||||||  |  || | |||||  | || || |
Db        360 ACAGTTACATATTTGTCATGATCCCTACCCTCTACAGCATCATCTTTGTGGTGGGAATAT 419

Qy        212 TTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCA 271
              ||||||||  ||   ||  |   |   |        |||  |  |||  |  | |   ||
Db        420 TTGGAAACAGCTTGGTGGTGATTGTCATTTACTTTTACATGAAGCTGAAGACTGTGGCCA 479

Qy        272 ACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAG 331
              |||  |||||  |||||  |   |||  | ||  ||    ||  || |  |   |
Db        480 GCGTCTTTCTTCTCAATCTCGCCTTGGCTGACTTATGCTTTTTGCTGACTTTGCCCCTGT 539

Qy        332 TCACACCATGGTACGCGATGACCAAAGACTGGGCATTCGG 371
                ||   |   |||  |||    |   ||||  | |||||
Db        540 GGGCAGTCTATACCGCTATGGAGTACCGCTGGCCCTTCGG 579


RESULT 15
US-11-136-527-2750
; Sequence 2750, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE:  2005-05-25
```

; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2750
; LENGTH: 1147
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2750

Query Match 4.0%; Score 47.6; DB 17; Length 1147;
Best Local Similarity 47.6%; Pred. No. 0.0062;
Matches 140; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

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Qy        170 TCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTAC 229
              || | | | |   |||  | | | |  |  |  | ||| |  |||| |||      |||
Db        155 TCCTTATACTGGCCTATTGTTCCATCATCTTGCTGGGCGTAGTTGGCAACTCTCTGGTAA 214

Qy        230 TATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACT 289
              |    | ||||   | |  |||| |  | |   | |    |||| | ||| |   ||||
Db        215 TCCATGTGGTGATCAAATTCAAGAGCATGCGCACAGTAACCAACTTTTTTATTGCCAACC 274

Qy        290 TGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGA 349
              ||    |  | ||| |  |  ||     |        | ||| |||| |      ||  |
Db        275 TGGCTGTGGCGGATCTTTTGGTGAACACCCTGTGCCTGCCATTCACTCTTACCTATACCT 334

Qy        350 TGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGT 409
              |||      || |||  | | ||  ||||  |||||||||| || || |   |  |
Db        335 TGATGGGGGAGTGGAAAATGGGTCCAGTTTTGTGCCATTTGGTGCCCTATGCCCAGGGTC 394

Qy        410 GTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTC 463
                | ||    ||| | |     |   | || |  ||  | || ||   |  ||
Db        395 TGGCAGTACAAGTGTCCACAATAACTTTGACAGTCATTGCTTTGGACCGACATC 448
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GenCore version 5.1.8

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Perfect score: 1193
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1193	100.0	1193	3	US-09-721-870-104	Sequence 104, App
2	1193	100.0	1500	3	US-09-721-870-39	Sequence 39, Appl
3	1109	93.0	1301	3	US-09-721-870-106	Sequence 106, App
4	96.6	8.1	1130	3	US-09-721-870-21	Sequence 21, Appl
5	84	7.0	1098	3	US-09-721-870-35	Sequence 35, Appl
6	78.8	6.6	1352	3	US-09-721-870-15	Sequence 15, Appl
7	66.6	5.6	1374	3	US-09-721-870-25	Sequence 25, Appl
8	61.6	5.2	1302	3	US-09-255-368-5	Sequence 5, Appli
9	61.6	5.2	1302	3	US-09-405-558-5	Sequence 5, Appli
10	61.6	5.2	1302	3	US-09-538-036-5	Sequence 5, Appli
11	61.6	5.2	1903	3	US-09-719-088B-4	Sequence 4, Appli
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13	57.8	4.8	1605	3	US-09-676-970-1	Sequence 1, Appli
14	57.8	4.8	1605	3	US-09-676-972B-1	Sequence 1, Appli
15	57.8	4.8	1605	3	US-09-016-434-1231	Sequence 1231, Ap
16	57.8	4.8	1605	3	US-09-676-941A-1	Sequence 1, Appli
17	57.8	4.8	1605	3	US-10-013-846-3	Sequence 3, Appli
18	57.8	4.8	1605	3	US-10-291-446-1	Sequence 1, Appli
19	57.8	4.8	1605	3	US-10-410-648-3	Sequence 3, Appli
20	57.8	4.8	2624	2	US-08-232-144-3	Sequence 3, Appli
21	57.8	4.8	2624	3	US-09-708-392-10	Sequence 10, Appl
22	57.8	4.8	4571	2	US-08-232-144-5	Sequence 5, Appli
23	56	4.7	1208	3	US-09-721-870-7	Sequence 7, Appli
24	56	4.7	1214	3	US-09-721-870-5	Sequence 5, Appli
25	56	4.7	1220	3	US-09-721-870-9	Sequence 9, Appli
26	56	4.7	1318	3	US-09-721-870-11	Sequence 11, Appl
27	54.4	4.6	1152	3	US-09-045-186-1	Sequence 1, Appli
28	54.4	4.6	1152	3	US-09-045-186-3	Sequence 3, Appli
29	53.4	4.5	1329	3	US-09-826-509-496	Sequence 496, App
30	53.4	4.5	1470	3	US-09-016-434-1203	Sequence 1203, Ap
31	53.4	4.5	1873	3	US-08-910-864-13	Sequence 13, Appl
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33	53.4	4.5	4301	3	US-09-931-157-2	Sequence 2, Appli
34	53.2	4.5	1163	3	US-09-721-870-13	Sequence 13, Appl
35	51.2	4.3	1155	3	US-09-053-866-3	Sequence 3, Appli
36	51.2	4.3	1155	3	US-09-479-130-3	Sequence 3, Appli
37	51.2	4.3	1155	3	US-09-472-130A-3	Sequence 3, Appli
38	50.6	4.2	1335	3	US-09-826-509-550	Sequence 550, App
39	50.6	4.2	1633	3	US-09-119-788-1	Sequence 1, Appli
40	50	4.2	1228	3	US-09-719-088B-5	Sequence 5, Appli
41	50	4.2	1410	3	US-09-255-368-1	Sequence 1, Appli
42	50	4.2	1410	3	US-09-405-558-1	Sequence 1, Appli
43	50	4.2	1410	3	US-09-538-036-1	Sequence 1, Appli
44	49.4	4.1	1754	3	US-09-693-746-21	Sequence 21, Appl
45	48.6	4.1	1321	3	US-09-175-658B-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-721-870-104
; Sequence 104, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Geary, Timothy G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/09/721,870
; CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 104
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1191)
; FEATURE:
; OTHER INFORMATION: Clone identifier: CEGPCR19.2
US-09-721-870-104

Query Match 100.0%; Score 1193; DB 3; Length 1193;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 60

Qy         61 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120

Qy        121 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 180

Qy        181 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 240

Qy        241 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 300
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Db        241 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 300

Qy        301 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 360

Qy        361 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 420

Qy        421 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC 480

Qy        481 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 540

Qy        541 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC 600

Qy        601 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 660

Qy        661 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 720

Qy        721 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 780

Qy        781 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 840

Qy        841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900

Qy        901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960

Qy        961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020

Qy       1021 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1080

Qy       1081 AACTCAACAGAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAGGGATCCAGCTACAC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AACTCAACAGAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAGGGATCCAGCTACAC 1140

Qy       1141 GACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 1193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 1193


RESULT 2
US-09-721-870-39
; Sequence 39, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Geary, Timothy G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 28341/6223
;  CURRENT APPLICATION NUMBER: US/09/721,870
;  CURRENT FILING DATE:  2000-11-24
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
;   LENGTH: 1500
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1497)
;   FEATURE:
;   OTHER INFORMATION: Clone identifier: CEGPCR19
US-09-721-870-39

  Query Match             100.0%;  Score 1193;  DB 3;  Length 1500;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1193;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 366

Qy         61 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 426

Qy        121 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 486

Qy        181 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 546

Qy        241 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 606

Qy        301 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 666

Qy        361 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 726

Qy        421 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC 786

Qy        481 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 846

Qy        541 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC 906

Qy        601 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 966

Qy        661 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 1026

Qy        721 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 1086
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Qy        781 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 1146

Qy        841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1147 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 1206

Qy        901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1207 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 1266

Qy        961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1267 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1326

Qy       1021 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1327 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1386

Qy       1081 AACTCAACAGAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAGGGATCCAGCTACAC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1387 AACTCAACAGAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAGGGATCCAGCTACAC 1446

Qy       1141 GACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 1193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 GACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACTCTTTCTA 1499
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RESULT 3
US-09-721-870-106
; Sequence 106, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Geary, Timothy G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/09/721,870
; CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 106
; LENGTH: 1301
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1299)
; FEATURE:
; OTHER INFORMATION: Clone identifier: CEGPCR19.1
US-09-721-870-106

Query Match 93.0%; Score 1109; DB 3; Length 1301;
Best Local Similarity 94.2%; Pred. No. 0;
Matches 1193; Conservative 0; Mismatches 0; Indels 74; Gaps 1;

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Qy          1 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTTAGTTCGGCGGCCACCATTTCGACCATTTCAACCACAACGACTCCCTCCACCATC 60

Qy         61 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGCAACGTTATCACAAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATT 120

Qy        121 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGGCACAAGGCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTC 180

Qy        181 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTG 240

Qy        241 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACC 300

Qy        301 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGAC 360

Qy        361 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTT 420

Qy        421 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCC 480

Qy        481 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTC 540

Qy        541 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTAC 600

Qy        601 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTTCAGCCCGGAGAAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGC 660

Qy        661 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAAAATAGTCGAAAGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATG 720

Qy        721 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCAGTGATCACGTATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATC 780

Qy        781 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAAAATGCTCAATTCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGA 840

Qy        841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900

Qy        901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960

Qy        961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020

Qy       1021 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCTCTGCTATTCTTTTGGCTGACACGAAAACAAAAACGTTCCGGACTGTCAAAAATACTC 1080

Qy       1081 AACTCAACAG---------------------------------------------------- 1090
              ||||||||||
Db       1081 AACTCAACAGAGATTGTGTCCTCGTTTGCCAGTAGAGTGAGTAACTCGATTCGGCGGTCA 1140

Qy       1091 ----------------------AGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAG 1126
                                      ||||||||||||||||||||||||||||||||||||
Db       1141 ACGTTTCGGAGAAACAATATTGACAGGGTTCGAAAAAAGCAGGTGGTTCTGGATTGCGAG 1200

Qy       1127 GGATCCAGCTACACGACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACT 1186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGATCCAGCTACACGACCTCCTCCCGACCTCTACTCATTCGGACAGATGTGCAGGCAACT 1260

Qy       1187 CTTTCTA 1193
              |||||||
Db       1261 CTTTCTA 1267
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RESULT 4
US-09-721-870-21
; Sequence 21, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Geary, Timothy G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 28341/6223
;  CURRENT APPLICATION NUMBER: US/09/721,870
;  CURRENT FILING DATE:  2000-11-24
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
;   LENGTH: 1130
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1128)
;   FEATURE:
;   OTHER INFORMATION: Clone identifier: CEGPCR4
US-09-721-870-21

  Query Match             8.1%;  Score 96.6;  DB 3;  Length 1130;
  Best Local Similarity   47.0%;  Pred. No. 1.3e-20;
  Matches  438;  Conservative    0;  Mismatches  454;  Indels   39;  Gaps    3;

Qy        136 GATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCCTG 195
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Db         52 GAAGATTTGTCATCAAGGTGGTACATAATGTTAGTGTTTGCATTTCTCTACCTGATAATC 111

Qy        196 TTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAAACAAGCGG 255
               |||      || ||  |||||||||    | ||  | | |||  |  | || |||||
Db        112 ATTGCCGCCGGAATAATTGGAAACTCATGTGTGATTTTGGCAATCACAAGGAACAAATCA 171

Qy        256 CTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATATTGGTG 315
              || ||| | | ||  ||  | ||| | ||    ||    |  | ||| | |  |
Db        172 CTTCAAACTGTTCCGAATCTGTTTATTCTTTCTTTATCATGTTCTGATATTGTGGTATGC 231

Qy        316 TTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGACTGGGCATTCGGGTCA 375
              | |||| |     || |||| ||       ||  | |  ||||| |||   || ||
Db        232 TGCACATCTGCAACAATCACTCCGATTACTGCATTCAAGAAAGAATGGATCTTTGGAGAG 291

Qy        376 GTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTTGTGACGAGTTGGAGC 435
              |   | ||||   | |  || ||       |         | | | |  | | ||  |
Db        292 GCTTTATGCCGAATTGCACCATTCATTGCTGGTATCAGCCTTTGTTTCTCAACTTTCACA 351

Qy        436 CTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCCACCAAACAACCAGTT 495
              | |||||||||||| | || | ||   | |  ||      ||| |  |   ||||  ||
Db        352 TTGACTGCAATCTCCATCGACAGATACATCCTGATTCGATTTCCGATGAGGAAACCTATT 411

Qy        496 TCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTCTCAACACTGATAAAT 555
              |   |  ||||||| | | | | |    | |||| ||      |  |  ||   || |
Db        412 ACGCATTATCAAGCGGTTGGAGTGATTGCTATTATTTGCGCTTTTGCTGCAACCATCA-- 469

Qy        556 CTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTACGTTCAGCCCGGAGAA 615
              |  |   ||  |||  |||| |||      |||  |||  |   |
Db        470 ----CATCCCCAATAATGTTCAAGCAAAAGCTGGGAGAGTTTGAGAAT------------ 513

Qy        616 ACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGCGAAAATAGTCGAAAG 675
                | ||  ||||| |  |||   ||      |   |  ||||      ||||
Db        514 ------TTTTGTGGGCAGTACTGCACGGAAAACTGGGGAGCCAATGAAAGCCAGAGAAAA 567

Qy        676 ATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATGGCAGTGATCACGTAT 735
              |||||  ||  |  |  | |||||  | ||| |||||  | |||  |  |  | ||||
Db        568 ATTTATGGTGCAGCTCTGATGTTTCTTCAGCTCGTCATTCCGCTTACCATCATCATCATA 627

Qy        736 TGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATCCAAAATGCTCAATTC 795
                | ||||      || |    ||  |  | ||  |||||  || ||   ||  ||
Db        628 TCCTACACTGCGATTTCTTTGAAGATCGGACAAAGCATGATTCTCAAAGGGGCGAAAAAG 687

Qy        796 TGTCAATCACTGA--------------CACAAAAGCAGAGAAGTGATGCGACGTCACGA 840
                || ||  |                |     | ||   |||   ||   |   ||
Db        688 CAAAAAACAGACAATTGGGAAATGGAATTAAGTGATCAACAAAGAATCGCTGTGAAGAGA 747

Qy        841 AAGAAGAAAGTGAATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTG 900
              |  | | |   |||   || || ||||  ||||| ||| ||||      |  | ||| |
Db        748 AGACAAAGAACTAATAGAATGCTTATTGGTATGGTAGTCGCATTCGCTTGCAGCTGGATT 807

Qy        901 CCTTTAACATTACTCAATTTGGTCAAAGATTTTAAAAAAGAGCCCGAATGGCTAAAACGT 960
                | |       ||||  |  | |  || | | || |   ||| ||      | |||  |
Db        808 TGGTCAGTGACGTTCAACATTCTGAGGGACTATGAATATTTGCCAGAGCTCATCAAAACT 867

Qy        961 CAGCCGTTCTTCTGGGCAATAAATGCTCACGTCATAGCCATGTCCTTAGTCGTCTGGAAC 1020
              ||    |  |||  | |||   | | ||   ||| || ||| ||| |   || ||||||
Db        868 CAAGAATATATCTTTGGAATTGCTACACATTGCATTGCAATGACCTCAACGGTATGGAAC 927

Qy       1021 CCTCTGCTATTCTTTTGGCTGACACGAAAAC 1051
              ||  | ||  | |      ||| |  |   |||
Db        928 CCGTTACTCTACGCAGTGCTCAACCTCCAAC 958


RESULT 5
US-09-721-870-35
; Sequence 35, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Geary, Timothy G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 28341/6223
;  CURRENT APPLICATION NUMBER: US/09/721,870
;  CURRENT FILING DATE:  2000-11-24
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
;   LENGTH: 1098
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1095)
;   FEATURE:
;   OTHER INFORMATION: Clone identifier: CEGPCR16
US-09-721-870-35

  Query Match             7.0%;  Score 84;  DB 3;  Length 1098;
  Best Local Similarity   50.5%;  Pred. No. 1.6e-16;
  Matches  204;  Conservative    0;  Mismatches  200;  Indels    0;  Gaps    0;

Qy        167 CAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCG 226
              | |||  |  ||  | |||||    |  |  | ||| | ||| |    || ||       |
Db         86 CGATTCTTGCAACCATCTACACTATAATTGTCGTAGTTGGCGTAACCGGCAATTTGTTAG 145

Qy        227 TACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCA 286
              ||  |  | |||||  |||   |||     || ||||| |   | ||| | ||  |  |
Db        146 TAGTGATGTCGGTGATGAGGTTCAAAGTTCTTCAATCAGTCAGGAACATGTTCATCGTAT 205

Qy        287 ACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACG 346
              |||    |  | ||  |  |  ||| | |       | |||| || ||       ||
Db        206 CTTTGTCAGTTTCTGACATTTTTGTGGCGATTGTTAGTGGTTCAGTAACGCCGATAACCG 265

Qy        347 CGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATT 406
              |  | | ||||  |||  ||| ||    |     |||| |||||| | |||||||  | |
Db        266 CATTCTCTAAAGTTTGGTTATTTGGTGGACCATTGTGTCATTTACTACCTTTGTTACAGG 325

Qy        407 CGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGC 466
                || ||  | |  | |  |  |  ||||| |||||  |  | || | || | | |
Db        326 GTACCGCGTTGAGTTTTTCCACGTTAACGCTCACCGCAATTGCAATTGACAGATATATTC 385
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Qy        467 ATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTC 526
              |||    |||| || ||| ||||  |    |  |||||| |||  ||| | |  |
Db        386 TCATCTGTCATCCGACGAAAGAACCGATACGCAAAGATCAAGCATTGAAAATGATAAGTT 445

Qy        527 TTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATG 570
              | | | |     |||||     | |     |||| |   | |||
Db        446 TCAACAGCGCCATCTCAGTTGGGCTTTCGGTACCATTATTCATG 489


RESULT 6
US-09-721-870-15
; Sequence 15, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Geary, Timothy G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 28341/6223
;  CURRENT APPLICATION NUMBER: US/09/721,870
;  CURRENT FILING DATE:  2000-11-24
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 1352
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1350)
;   FEATURE:
;   OTHER INFORMATION: Clone identifier: CEGPCR14
US-09-721-870-15

  Query Match             6.6%;  Score 78.8;  DB 3;  Length 1352;
  Best Local Similarity   47.4%;  Pred. No. 9.2e-15;
  Matches  381;  Conservative    0;  Mismatches  402;  Indels   21;  Gaps    4;

Qy        134 TCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCC 193
              || |||||   || ||   |||| | | ||       |   || | || |||    ||
Db         56 TCAATGATTGGACAGTCCTCTTTGAAGTTCGGCTTGGATATTCAGTACTATACTTTCTCA 115

Qy        194 TGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAAACAAGC 253
              | ||  || | ||  |  |||||||  ||      |  |      |  |      |||
Db        116 TATTAATAATCGGATTGGTTGGAAATGGGCTATTGATCACTTCAATTTTAATGCGAAAGA 175

Qy        254 GGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATATTGG 313
                ||      |||    ||| |||| || | ||| ||    |  | ||||||  |  |
Db        176 AACTTTCCGTGGC---AAACATATTCTTGATAAACCTGGCAGTTTCTGATTTGCTTCTTT 232

Qy        314 TGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGACTGGGCATTCGGGT 373
              ||||  |||  | ||  |||| |||   | ||| | |  ||    |||  ||| ||
Db        233 GCATCACGGCGGTGCCGATCACTCCAGTATTGGCGTTTATGAAGCGATGGATATTTGGAA 292

Qy        374 CAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTTGTGACGAGTTGGA 433
              | | ||||  | || ||||     |   | ||| |||||||  |   |  |     |||
Db        293 TAATTATGTGTAAATTGGTTCCAACTTGTCAGGCGTTTTCGGTGCTCATTTCTTCATGGT 352

Qy        434 GCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCCACCAAACAACCAG 493
              |    |   ||| |  | |||| || ||    |||        ||   |   |||||
Db        353 CTTTGTGTTACATCGCAATTGATAGATATCGAAGTATTGTGACGCCACTCCGGGAACCAT 412

Qy        494 TTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTCTCAACACTGATAA 553
              |||  | | || ||   |    |   | | |  ||| | ||| |    ||    |
Db        413 GGTCTGATAGGCATGCAAGGTGGCTTCTGATGTTCACATGGGTGGTCGCCTTCCTTGCTA 472

Qy        554 ATCTACCGTATCTTATGTCTTTCGAGCACGTCGATGGAAGCTTTTACGTTCAGCCCGGAG 613
              |      |||| | | | || |   ||  |      ||   |      || |       |
Db        473 GT------TATCCTCTATATTACTCACAGAACTTGAAAACAATGGTTATTGA------AA 520

Qy        614 AAACTCCATACTGCGGGCACTTTTGCGACGAGGCGAATTGGCAGAGCGAAAATAGTCGAA 673
              |      |||  || ||  | |||||| ||||   |||||||||   ||  | |     |
Db        521 ATGTGACATTATGTGGAGATTTTTGCGGCGAGTTCAATTGGCAGTCGGATGAAATATCCA 580

Qy        674 AGATTTACGGAACTACGGTTATGTTGTTACAGTTCGTCGTGCCGATGGCAGTGATCACGT 733
              || |       ||||||  | | ||| |       |  |       ||| | |||| ||
Db        581 AGTTGACATATACTACGAGTTTATTGATTATTCAGCTGATTATTCCAGCAATTATCATGT 640

Qy        734 ATTGCTACTTCAAAATCTTGCAAAAAGTGTCAAAAGACATGATCATCCAAAATGCTCAAT 793
              ||  |  |   |||  | | | ||  | | ||  |      |    | |    ||
Db        641 CTTTTTGTTATTTAATGATTCTACAAAAGGTACAAACCGACTGGCTTGTCGACGAGGGAT 700

Qy        794 TCTGTCAATCACTGACACAAAAGCAGAGAAGTGATGCGACGTCACGAAAGAAGAAAGTGA 853
              |       |     ||||| ||     ||  |  |       ||||||     |||||
Db        701 CCATGTTGACTGCCGCACAACAGGCTCAAACAGCAG------TTCGAAAGCGACGAGTGA 754

Qy        854 ATTATATTCTAATTGCAATGGTTGTCACATTTATCGGGTGTTGGTTGCCTTTAACATTAC 913
                ||  |  | |||  ||||||| |   |||||  |  || ||||| || ||  |
Db        755 TGTACGTGTTGATTCTAATGGTTATTGTTTTTATGGCTTGCTGGTTCCCGTTGTCCGCCG 814

Qy        914 TCAATTTGGTCAAAGATTTTAAAA 937
              | |||||| ||| |||| |   ||
Db        815 TGAATTTGTTCAGAGATCTCGGAA 838


RESULT 7
US-09-721-870-25
; Sequence 25, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Geary, Timothy G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 28341/6223
;  CURRENT APPLICATION NUMBER: US/09/721,870
;  CURRENT FILING DATE:  2000-11-24
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
;   LENGTH: 1374
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1371)
;   FEATURE:
;   OTHER INFORMATION: Clone identifier: CEGPCR7
US-09-721-870-25

  Query Match             5.6%;  Score 66.6;  DB 3;  Length 1374;
  Best Local Similarity   48.3%;  Pred. No. 8.9e-11;
  Matches  186;  Conservative    0;  Mismatches  199;  Indels    0;  Gaps    0;

Qy        180 CCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGT 239
              | | |||   || || ||| |  | ||  | |||||||| |    |  | |  |  |
Db         93 CGTGTACCTTTTTCTCTTTTTTCTTGGACTCTTTGGAAATGTGACCTTGATTTACGTAAC 152

Qy        240 GGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCAC 299
                 ||  | ||     | |     | ||  ||| |||| | || ||| ||      |
Db        153 TTGCAGCCATAAAGCTTTACTGAGCGTTCAAAACATATTCATTCTGAACCTGGCGGCGAG 212

Qy        300 CGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGA 359
              |||||  ||  ||     |  | ||| |||| |||           ||  |||| |
Db        213 CGATTGCATGATGTGCATATTATCGCTTCCAATCACTCCAATCACAAATGTGTACAAAAA 272

Qy        360 CTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTT 419
              ||||   || ||     |  | ||||||||  | || |     |          | ||
Db        273 CTGGTACTTTGGAAATCTACTCTGCCATTTGATACCATGCATTCAAGGTATCAGCATTTT 332

Qy        420 TGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCC 479
              ||    |  |  || ||| ||| ||  | || |||   | | | | | |        ||
Db        333 CGTATGCACATTCAGTCTCGGTGCGATTGCTTTGGATCGGTATATCCTTGTAGTAAGACC 392
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Qy        480 CACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGT 539
              |||| | ||   |  ||| ||   |  ||  ||||  | |||||  |
Db        393 ACATTCTACACCACTATCCCAAAGAGGAGCATTTCTTACTACTGTTCTATTGTGGATCCT 452

Qy        540 CTCAACACTGATAAATCTACCGTAT 564
              |||     |  ||| ||||||| |||
Db        453 CTCTTTTGTTGTAACTCTACCCTAT 477


RESULT 8
US-09-255-368-5
; Sequence 5, Application US/09255368
; Patent No. 6262246
; GENERAL INFORMATION:
;  APPLICANT: Gerald, Christophe P.G.
;  APPLICANT: Jones, Kenneth A.
;  APPLICANT: Bonini, James A.
;  APPLICANT: Borowsky, Beth
;  TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
;  TITLE OF INVENTION: and Uses Thereof
;  FILE REFERENCE: 1795/57155-A
;  CURRENT APPLICATION NUMBER: US/09/255,368
;  CURRENT FILING DATE: 1999-02-22
;  EARLIER APPLICATION NUMBER: 09/161,113
;  EARLIER FILING DATE: 1998-09-25
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 5
;   LENGTH: 1302
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-255-368-5

  Query Match             5.2%;  Score 61.6;  DB 3;  Length 1302;
  Best Local Similarity   46.3%;  Pred. No. 3.7e-09;
  Matches  202;  Conservative    0;  Mismatches  234;  Indels    0;  Gaps    0;

Qy        165 ATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGG 224
              | |||||||||    |   ||||    |  | ||  | ||  ||||  | |||||    |
Db        165 AGCAATCTTCATTATTTCCTACTTTCTGATCTTCTTTTTGTGCATGATGGGAAATACTGT 224

Qy        225 CGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT 284
              ||     |     ||   ||| |||||  |   | ||  | |     ||  | ||  |  |
Db        225 GGTTTGCTTTATTGTAATGAGGAACAAACATATGCACACAGTCACTAATCTCTTCATCTT 284

Qy        285 CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTA 344
              |||  ||  | | |  |||||  ||  | |   |        ||  ||  | ||||    | |
Db        285 AAACCTGGCCATAAGTGATTTACTAGTTGGCATATTCTGCATGCCTATAACACTGCTGGA 344

Qy        345 CGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAA 404
              |   ||  |    ||  ||| |||| ||       |||||| |  |   |  |||    |
Db        345 CAATATTATAGCAGGATGGCCATTTGGAAACACGATGTGCAAGATCAGTGGATTGGTCCA 404

Qy        405 TTCGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCT 464
                 ||  ||     |   |   |    ||||||  |  ||||||  || |
Db        405 GGGAATATCTGTCGCAGCTTCAGTCTTTACGTTAGTTGCAATTGCTGTAGATAGGTTCCA 464

Qy        465 GCATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATT 524
              |  | |   | |  ||    |||| |    |  ||||      ||||||  |  ||  |
Db        465 GTGTGTGGTCTACCCTTTTAAACCAAAGCTCACTATCAAGACAGCGTTTGTCATTATTAT 524

Qy        525 TCTTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGT 584
              | |||||| |  |  | |     || |    || | |    |    ||  |
Db        525 GATCATCTGGGTCCTAGCCATCACCATTATGTCTCCATCTGCAGTAATGTTACATGTGCA 584

Qy        585 CGATGGAAGCTTTTAC 600
              || | ||  | ||||
Db        585 AGAAGAAAAATATTAC 600


RESULT 9
US-09-405-558-5
; Sequence 5, Application US/09405558A
; Patent No. 6709831
; GENERAL INFORMATION:
;  APPLICANT: Gerald, Christophe P.G.
;  APPLICANT: Jones, Kenneth A.
;  APPLICANT: Bonini, James A.
;  APPLICANT: Borowsky, Beth E.
;  APPLICANT: Craig, Douglas A.
;  TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
;  TITLE OF INVENTION: and Uses Thereof
;  FILE REFERENCE: 57155-C
;  CURRENT APPLICATION NUMBER: US/09/405,558A
;  CURRENT FILING DATE: 1999-09-24
;  EARLIER APPLICATION NUMBER: 09/161,113
;  EARLIER FILING DATE: 1998-09-25
;  EARLIER APPLICATION NUMBER: 09/255,368
;  EARLIER FILING DATE: 1999-02-22
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 5
;   LENGTH: 1302
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-405-558-5

  Query Match             5.2%;  Score 61.6;  DB 3;  Length 1302;
  Best Local Similarity   46.3%;  Pred. No. 3.7e-09;
  Matches  202;  Conservative    0;  Mismatches  234;  Indels    0;  Gaps    0;

Qy        165 ATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGG 224
              | |||||||||    |   ||||    |  | ||  | ||  ||||  | |||||    |
Db        165 AGCAATCTTCATTATTTCCTACTTTCTGATCTTCTTTTTGTGCATGATGGGAAATACTGT 224

Qy        225 CGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT 284
              ||     |     ||   ||| |||||  |   | ||  | |     ||  | ||  |  |
Db        225 GGTTTGCTTTATTGTAATGAGGAACAAACATATGCACACAGTCACTAATCTCTTCATCTT 284

Qy        285 CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTA 344
              |||  ||  | | |  |||||  ||  | |   |        ||  ||  | ||||    | |
Db        285 AAACCTGGCCATAAGTGATTTACTAGTTGGCATATTCTGCATGCCTATAACACTGCTGGA 344

Qy        345 CGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAA 404
              |   ||  |    ||  ||| |||| ||       |||||| |  |   |  |||    |
Db        345 CAATATTATAGCAGGATGGCCATTTGGAAACACGATGTGCAAGATCAGTGGATTGGTCCA 404

Qy        405 TTCGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCT 464
                 ||  ||     |   |   |    ||||||  |  ||||||  || |
Db        405 GGGAATATCTGTCGCAGCTTCAGTCTTTACGTTAGTTGCAATTGCTGTAGATAGGTTCCA 464

Qy        465 GCATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATT 524
              |  | |   | |  ||    |||| |    |  ||||      ||||||  |  ||  |
Db        465 GTGTGTGGTCTACCCTTTTAAACCAAAGCTCACTATCAAGACAGCGTTTGTCATTATTAT 524

Qy        525 TCTTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGT 584
              | |||||| |  |  | |     || |    || | |    |    ||  |
Db        525 GATCATCTGGGTCCTAGCCATCACCATTATGTCTCCATCTGCAGTAATGTTACATGTGCA 584

Qy        585 CGATGGAAGCTTTTAC 600
              || | ||  | ||||
Db        585 AGAAGAAAAATATTAC 600


RESULT 10
US-09-538-036-5
; Sequence 5, Application US/09538036
; Patent No. 6849727
; GENERAL INFORMATION:
;  APPLICANT: Gerald, Christophe P.G.
;  APPLICANT: Jones, Kenneth A.
;  APPLICANT: Bonini, James A.
;  APPLICANT: Borowsky, Beth E.
;  APPLICANT: Craig, Douglas A.
;  TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
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;  TITLE OF INVENTION: And Uses Thereof
;  FILE REFERENCE: 57155-D/JPW
;  CURRENT APPLICATION NUMBER: US/09/538,036
;  CURRENT FILING DATE: 2000-03-29
;  EARLIER APPLICATION NUMBER: 09/405,558
;  EARLIER FILING DATE: 1999-09-24
;  EARLIER APPLICATION NUMBER: 09/255,368
;  EARLIER FILING DATE: 1999-02-22
;  EARLIER APPLICATION NUMBER: 09/161,113
;  EARLIER FILING DATE: 1998-09-25
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 1302
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-538-036-5

  Query Match             5.2%;  Score 61.6;  DB 3;  Length 1302;
  Best Local Similarity   46.3%;  Pred. No. 3.7e-09;
  Matches  202;  Conservative    0;  Mismatches  234;  Indels    0;  Gaps    0;

Qy        165 ATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGG 224
              | |||||||||    |   ||||    |  | ||  | ||  ||||  | |||||    |
Db        165 AGCAATCTTCATTATTTCCTACTTTCTGATCTTCTTTTTGTGCATGATGGGAAATACTGT 224

Qy        225 CGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT 284
              ||     |     ||   ||| ||||| |   | ||  | |      ||  | ||  |  |
Db        225 GGTTTGCTTTATTGTAATGAGGAACAAACATATGCACACAGTCACTAATCTCTTCATCTT 284

Qy        285 CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTA 344
              |||  ||  | | |  |||||  || | |   |        || ||  | ||||    | |
Db        285 AAACCTGGCCATAAGTGATTTACTAGTTGGCATATTCTGCATGCCTATAACACTGCTGGA 344

Qy        345 CGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAA 404
              |   || |   ||  ||| |||| ||      |||||| | |   |   |||    |
Db        345 CAATATTATAGCAGGATGGCCATTTGGAAACACGATGTGCAAGATCAGTGGATTGGTCCA 404

Qy        405 TTCGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCT 464
              ||  ||    |   |    |  |   |  ||||||  |  ||||||  ||  |
Db        405 GGGAATATCTGTCGCAGCTTCAGTCTTTACGTTAGTTGCAATTGCTGTAGATAGGTTCCA 464

Qy        465 GCATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATT 524
              |  | |   | | ||    |||| |    |  ||||      |||||| |  || |   |
Db        465 GTGTGTGGTCTACCCTTTTAAACCAAAGCTCACTATCAAGACAGCGTTTGTCATTATTAT 524

Qy        525 TCTTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGT 584
              | ||||||  |  |  | |     || |    || | |    |    ||  |
Db        525 GATCATCTGGGTCCTAGCCATCACCATTATGTCTCCATCTGCAGTAATGTTACATGTGCA 584

Qy        585 CGATGGAAGCTTTTAC 600
              || | ||  | ||||
Db        585 AGAAGAAAAATATTAC 600


RESULT 11
US-09-719-088B-4
; Sequence 4, Application US/09719088B
; Patent No. 6803232
; GENERAL INFORMATION:
;  APPLICANT: Herzog, Herbert
;  TITLE OF INVENTION: NPY-Y7 Receptor Gene
;  FILE REFERENCE: 12020-0003
;  CURRENT APPLICATION NUMBER: US/09/719,088B
;  CURRENT FILING DATE:  2000-12-08
;  PRIOR APPLICATION NUMBER: PCT/AU99/00523
;  PRIOR FILING DATE: 1999-06-29
;  PRIOR APPLICATION NUMBER: AU PP4385
;  PRIOR FILING DATE: 1998-06-29
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 1903
;   TYPE: DNA
;   ORGANISM: Homo sapiens NPY-Y7-encoding gene
US-09-719-088B-4

  Query Match             5.2%;  Score 61.6;  DB 3;  Length 1903;
  Best Local Similarity   46.3%;  Pred. No. 4.7e-09;
  Matches  202;  Conservative    0;  Mismatches  234;  Indels    0;  Gaps    0;

Qy        165 ATCAATCTTCACATTCCTCTACGGGTTCCTGTTTGTATTAGGCATTTTTGGAAACGGCGG 224
              | |||||||||    |   ||||    |  | ||  | ||  ||||  | |||||    |
Db        512 AGCAATCTTCATTATTTCCTACTTTCTGATCTTCTTTTTGTGCATGATGGGAAATACTGT 571

Qy        225 CGTACTATGGGCGGTGGCGAGAAACAAGCGGCTCCAATCGGCTCGCAACGTATTTCTGCT 284
              ||     |     ||   ||| ||||| |   | ||  | |      ||  | ||  |  |
Db        572 GGTTTGCTTTATTGTAATGAGGAACAAACATATGCACACAGTCACTAATCTCTTCATCTT 631

Qy        285 CAACTTGATCTTCACCGATTTGATATTGGTGTTCACAGCGATTCCAGTCACACCATGGTA 344
              |||  ||  | | |  |||||  || | |   |        || ||  | ||||    | |
Db        632 AAACCTGGCCATAAGTGATTTACTAGTTGGCATATTCTGCATGCCTATAACACTGCTGGA 691

Qy        345 CGCGATGACCAAAGACTGGGCATTCGGGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAA 404
              |   || |   ||  ||| |||| ||      |||||| | |   |   |||    |
Db        692 CAATATTATAGCAGGATGGCCATTTGGAAACACGATGTGCAAGATCAGTGGATTGGTCCA 751

Qy        405 TTCGTGTTCGGTGTTTGTGACGAGTTGGAGCCTCACTGCAATCTCCTTAGATAAATTTCT 464
              ||  ||    |   |    |  |   |  ||||||  |  ||||||  ||  |
Db        752 GGGAATATCTGTCGCAGCTTCAGTCTTTACGTTAGTTGCAATTGCTGTAGATAGGTTCCA 811

Qy        465 GCATATCAACGATCCCACCAAACAACCAGTTTCTATTCGTCAAGCGTTGGCAATAACATT 524
              |  | |   | | ||    |||| |    |  ||||      |||||| |  || |   |
Db        812 GTGTGTGGTCTACCCTTTTAAACCAAAGCTCACTATCAAGACAGCGTTTGTCATTATTAT 871

Qy        525 TCTTATCTGGATAGTCTCAACACTGATAAATCTACCGTATCTTATGTCTTTCGAGCACGT 584
              | ||||||  |  |  | |     || |    || | |    |    ||  |
Db        872 GATCATCTGGGTCCTAGCCATCACCATTATGTCTCCATCTGCAGTAATGTTACATGTGCA 931

Qy        585 CGATGGAAGCTTTTAC 600
              || | ||  | ||||
Db        932 AGAAGAAAAATATTAC 947


RESULT 12
US-09-693-746-1
; Sequence 1, Application US/09693746
; Patent No. 6835546
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Smith, Valdin G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Metho
;  TITLE OF INVENTION:  Related To The Same
;  FILE REFERENCE: 6297.1cp
;  CURRENT APPLICATION NUMBER: US/09/693,746
;  CURRENT FILING DATE:  2000-10-20
;  PRIOR APPLICATION NUMBER: 09/425,676
;  PRIOR FILING DATE: 1999-10-22
;  NUMBER OF SEQ ID NOS: 168
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1803
;   TYPE: DNA
;   ORGANISM: D. melanogaster
US-09-693-746-1

  Query Match             5.0%;  Score 60.2;  DB 3;  Length 1803;
  Best Local Similarity   45.9%;  Pred. No. 1.3e-08;
  Matches  206;  Conservative    0;  Mismatches  243;  Indels    0;  Gaps    0;

Qy        131 GCATCGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGT 190
              | | ||  |  || | |    ||   | | | |    |||||   |||| ||||
Db        155 GGAGCGGCGGGATCATTCACAACCAGTTCGTGCAAATCTTCTTCTACGTCCTGTACGCCA 214
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Qy        191 TCCTGTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAAACA 250
Db        215 CGGTCTTTGTCCTGGGTGTCTTCGGAAATGTCCTGGTTTGCTACGTAGTTCTGAGGAATC 274

Qy        251 AGCGGCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATAT 310
Db        275 GGGCCATGCAGACTGTGACCAATATATTCATCACGAATCTGGCCCTGTCGGACATATTGC 334

Qy        311 TGGTGTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGACTGGGCATTCG 370
Db        335 TCTGCGTCCTGGCGGTGCCATTTACTCCGCTTTACACGTTCATGGGTCGCTGGGCCTTCG 394

Qy        371 GGTCAGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTTGTGACGAGTT 430
Db        395 GCAGGAGTCTGTGCCATCTGGTGTCCTTTGCCCAGGGATGCAGCATCTACATATCCACGC 454

Qy        431 GGAGCCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCCCACCAAACAAC 490
Db        455 TGACCCTCACCTCGATTGCCATCGATCGGTACTTCGTTATCATATACCCCTTCCATCCGC 514

Qy        491 CAGTTTCTATTCGTCAAGCGTTGGCAATAACATTTCTTATCTGGATAGTCTCAACACTGA 550
Db        515 GCATGAAGCTCTCCACCTGCATCGGGATCATAGTGAGCATCTGGGTGATAGCCCTGCTGG 574

Qy        551 TAAATCTACCGTATCTTATGTCTTTCGAG 579
Db        575 CCACCGTTCCCTACGGCATGTACATGAAG 603
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RESULT 13
US-09-676-970-1
; Sequence 1, Application US/09676970
; Patent No. 6372743
; GENERAL INFORMATION:
; APPLICANT: Darrow, James W.
; APPLICANT: De Lombaert, Stephane
; APPLICANT: Blum, Charles
; APPLICANT: Tran, Jennifer
; APPLICANT: Giangiordano, Mark
; APPLICANT: Griffith, David Andrew
; APPLICANT: Carpino, Philip Albert
; TITLE OF INVENTION: Certain Alkylene Diamine-Substituted Pyrazolo
; TITLE OF INVENTION: [1,5,-a]-1,5-Pyrimidines and pyrazolo
; TITLE OF INVENTION: [1,5-a]-1,3,5-Triazines
; FILE REFERENCE: U012955-3
; CURRENT APPLICATION NUMBER: US/09/676,970
; CURRENT FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-676-970-1

Query Match 4.8%; Score 57.8; DB 3; Length 1605;
Best Local Similarity 46.4%; Pred. No. 7.3e-08;
Matches 188; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

```
Qy         75 AAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATTGCGGCACAAGGCAT 134
Db        226 AAATCATTCAGTCCACTCTAATTTCTCAGAGAAGAATGCCCAGCTTCTGGCTTTTGAAAA 285

Qy        135 CGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCCT 194
Db        286 TGATGATTGTCATCTGCCCTTGGCCATGATATTTACCTTAGCTCTTGCTTATGGAGCTGT 345

Qy        195 GTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAAACAAGCG 254
Db        346 GATCATTCTTGGTGTCTCTGGAAACCTGGCCTTGATCATAATCATCTTGAAACAAAAGGA 405

Qy        255 GCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATATTGGT 314
Db        406 GATGAGAAATGTTACCAACATCCTGATTGTGAACCTTTCCTTCTCAGACTTGCTTGTTGC 465

Qy        315 GTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGACTGGGCATTCGGGTC 374
Db        466 CATCATGTGTCTCCCCTTTACATTTGTCTACACATTAATGGACCACTGGGTCTTTGGTGA 525

Qy        375 AGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTTGTGACGAGTTGGAG 434
Db        526 GGCGATGTGTAAGTTGAATCCTTTTGTGCAATGTGTTTCAATCACTGTGTCCATTTTCTC 585

Qy        435 CCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCC 479
Db        586 TCTGGTTCTCATTGCTGTGGAACGACATCAGCTGATAATCAACCC 630
```

RESULT 14
US-09-676-972B-1
; Sequence 1, Application US/09676972B
; Patent No. 6476038
; GENERAL INFORMATION:
; APPLICANT: Darrow, James W.
; APPLICANT: De Lombaert, Stephane
; APPLICANT: Blum, Charles
; APPLICANT: Tran, Jennifer
; APPLICANT: Giangiordano, Mark
; APPLICANT: Griffith, David Andrew
; APPLICANT: Carpino, Philip Albert
; TITLE OF INVENTION: Amino Substituted Pyrazolo [1,5,-a]-1,5-Pyrimidines and
; TITLE OF INVENTION: Pyrazolo [1,5-a]-1,3,5-Triazines
; FILE REFERENCE: U 012956-1
; CURRENT APPLICATION NUMBER: US/09/676,972B
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/156,868
; PRIOR FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-676-972B-1

Query Match 4.8%; Score 57.8; DB 3; Length 1605;
Best Local Similarity 46.4%; Pred. No. 7.3e-08;
Matches 188; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

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Qy         75 AAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATTGCGGCACAAGGCAT 134
Db        226 AAATCATTCAGTCCACTCTAATTTCTCAGAGAAGAATGCCCAGCTTCTGGCTTTTGAAAA 285

Qy        135 CGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCCT 194
Db        286 TGATGATTGTCATCTGCCCTTGGCCATGATATTTACCTTAGCTCTTGCTTATGGAGCTGT 345

Qy        195 GTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAAACAAGCG 254
Db        346 GATCATTCTTGGTGTCTCTGGAAACCTGGCCTTGATCATAATCATCTTGAAACAAAAGGA 405

Qy        255 GCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATATTGGT 314
Db        406 GATGAGAAATGTTACCAACATCCTGATTGTGAACCTTTCCTTCTCAGACTTGCTTGTTGC 465

Qy        315 GTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGACTGGGCATTCGGGTC 374
Db        466 CATCATGTGTCTCCCCTTTACATTTGTCTACACATTAATGGACCACTGGGTCTTTGGTGA 525

Qy        375 AGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTTGTGACGAGTTGGAG 434
Db        526 GGCGATGTGTAAGTTGAATCCTTTTGTGCAATGTGTTTCAATCACTGTGTCCATTTTCTC 585

Qy        435 CCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCC 479
Db        586 TCTGGTTCTCATTGCTGTGGAACGACATCAGCTGATAATCAACCC 630
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```
RESULT 15
US-09-016-434-1231
; Sequence 1231, Application US/09016434
; Patent No. 6500938
;  GENERAL INFORMATION:
;    APPLICANT:  Janice Au-Young
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF SIGNALING
;    TITLE OF INVENTION:  PATHWAY GENE EXPRESSION
;    NUMBER OF SEQUENCES:  1490
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,434
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0002 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1231:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1605 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g189155
US-09-016-434-1231

  Query Match             4.8%;  Score 57.8;  DB 3;  Length 1605;
  Best Local Similarity   46.4%;  Pred. No. 7.3e-08;
  Matches  188;  Conservative    0;  Mismatches  217;  Indels    0;  Gaps    0;

Qy          75 AAGTCATTCGAACAATGGCTCGTGCATTCAGATCGCTGAGGCGATTGCGGCACAAGGCAT 134
               || ||||||   | |       | |    |||    ||    | ||  |||    |  |
Db         226 AAATCATTCAGTCCACTCTAATTTCTCAGAGAAGAATGCCCAGCTTCTGGCTTTTGAAAA 285

Qy         135 CGATGATATTACTGTAGACTTTTACATCCGATCAATCTTCACATTCCTCTACGGGTTCCT 194
                ||||||  |  | |  |||  |||  ||  | |||  |  |    || ||     |
Db         286 TGATGATTGTCATCTGCCCTTGGCCATGATATTTACCTTAGCTCTTGCTTATGGAGCTGT 345

Qy         195 GTTTGTATTAGGCATTTTTGGAAACGGCGGCGTACTATGGGCGGTGGCGAGAAACAAGCG 254
               | |  |  | ||  | | ||||||   | | |  |         |   || | | |||
Db         346 GATCATTCTTGGTGTCTCTGGAAACCTGGCCTTGATCATAATCATCTTGAAACAAAAGGA 405

Qy         255 GCTCCAATCGGCTCGCAACGTATTTCTGCTCAACTTGATCTTCACCGATTTGATATTGGT 314
               | |    |   | |  |||| |  |  |  | ||| |   ||||  | || ||| |  | |
Db         406 GATGAGAAATGTTACCAACATCCTGATTGTGAACCTTTCCTTCTCAGACTTGCTTGTTGC 465

Qy         315 GTTCACAGCGATTCCAGTCACACCATGGTACGCGATGACCAAAGACTGGGCATTCGGGTC 374
                 |||     | ||  | |||      ||| |  | |   |  ||||||  || ||
Db         466 CATCATGTGTCTCCCCTTTACATTTGTCTACACATTAATGGACCACTGGGTCTTTGGTGA 525

Qy         375 AGTGATGTGCCATTTAGTTCCTTTGTCAAATTCGTGTTCGGTGTTTGTGACGAGTTGGAG 434
               | ||||||  | ||   ||||||      | |    |||  |   |||| | | ||
Db         526 GGCGATGTGTAAGTTGAATCCTTTTGTGCAATGTGTTTCAATCACTGTGTCCATTTTCTC 585

Qy         435 CCTCACTGCAATCTCCTTAGATAAATTTCTGCATATCAACGATCC 479
               ||   |   ||  |  | ||   |  || ||  || | | | ||
Db         586 TCTGGTTCTCATTGCTGTGGAACGACATCAGCTGATAATCAACCC 630


Search completed: May  8, 2006, 14:48:09
Job time : 257 secs
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OM protein - protein search, using sw model

Run on: May 8, 2006, 09:29:53 ; Search time 41 Seconds
(without alignments)
931.660 Million cell updates/sec

Title: US-10-650-467-105
Perfect score: 2074
Sequence: 1 MVSSAATISTISTTTTPSTI.....QLHDLLPTSTHSDRCAGNSF 397

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	607.5	29.3	539	2	T27559	hypothetical prote
2	514	24.8	374	2	T19340	hypothetical prote
3	485.5	23.4	457	2	T29741	hypothetical prote
4	461.5	22.3	365	2	T20184	hypothetical prote
5	419.5	20.2	412	2	T22076	hypothetical prote
6	387.5	18.7	373	2	T24487	hypothetical prote
7	382	18.4	376	2	T19186	hypothetical prote
8	373.5	18.0	370	1	I52315	G protein-coupled
9	354	17.1	375	2	S63685	neuropeptide Y rec
10	346.5	16.7	384	2	A45490	neuropeptide Y/pep
11	342	16.5	382	2	S27388	neuropeptide Y rec
12	337	16.2	449	2	A41738	neuropeptide Y rec
13	333	16.1	349	2	S12863	G protein-coupled
14	333	16.1	382	2	B46133	neuropeptide Y/pep
15	324	15.6	381	2	I39187	neuropeptide Y/pep
16	321	15.5	399	2	T16277	hypothetical prote
17	314	15.1	375	2	G02300	pancreatic polypep
18	314	15.1	375	2	I39182	neuropeptide Y/pep
19	310.5	15.0	366	2	S71152	neuropeptide Y/pep
20	305.5	14.7	504	2	A41783	tachykinin recepto
21	303.5	14.6	423	2	B40470	glucocorticoid-ind
22	295.5	14.2	391	2	T32714	hypothetical prote
23	292.5	14.1	391	2	C41795	somatostatin recep
24	292	14.1	428	2	S30508	probable G protein
25	290.5	14.0	443	2	D40470	glucocorticoid-ind
26	289	13.9	418	2	A46226	somatostatin recep
27	289	13.9	428	2	A44021	somatostatin recep
28	288.5	13.9	390	2	B41007	bombesin receptor,
29	286.5	13.8	391	2	A39297	somatostatin recep
30	284.5	13.7	391	2	A41795	somatostatin recep
31	284.5	13.7	423	2	JC7677	allatostatin recep
32	283.5	13.7	376	2	I50102	Phe13 bombesin rec
33	282.5	13.6	455	2	T15622	hypothetical prote
34	282	13.6	391	2	T32517	hypothetical prote
35	281.5	13.6	369	2	B41795	somatostatin recep
36	281	13.5	363	2	I57940	somatostatin recep
37	281	13.5	519	2	S17783	tachykinin recepto
38	280.5	13.5	349	2	I59336	galanin receptor 1
39	279.5	13.5	384	2	S20303	neurokinin 2 recep
40	279.5	13.5	385	2	S55524	neurokinin 3 recep
41	278	13.4	346	2	S29248	somatostatin recep
42	277.5	13.4	440	2	A44081	kappa-type opioid
43	276.5	13.3	384	2	A47249	brain-specific som
44	276.5	13.3	388	2	JN0605	somatostatin recep
45	276.5	13.3	394	2	JC7209	galanin receptor -

ALIGNMENTS

RESULT 1
T27559
hypothetical protein ZC412.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27559
R;Ainscough, R.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z20387
A;Accession: T27559
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-539 <WIL>
A;Cross-references: UNIPROT:Q23305; UNIPARC:UPI0000083344; EMBL:Z78067; PIDN:CAB01528.1
A;Experimental source: clone ZC412
C;Genetics:
A;Gene: CESP:ZC412.1
A;Map position: 5
A;Introns: 29/3; 75/3; 112/1; 144/3; 180/3; 223/3; 241/3; 324/3; 376/2; 426/2; 456/3

Query Match 29.3%; Score 607.5; DB 2; Length 539;
Best Local Similarity 35.3%; Pred. No. 7.6e-44;
Matches 119; Conservative 76; Mismatches 111; Indels 31; Gaps 7;

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Qy         33 CIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNV 92
              || :   :  |  :| || | :|  :: ||  : ::|: ||| :: ::   |:| |  |:
Db          9 CIDVNAIL--QQFNDWTVLFEVRLGYSVLYFLILIIGLVGNGLLITSILMRKKL-SVANI 65

Qy         93 FLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLD 152
              ||:||  :||:|  ||:|:||  |  | | || :|| |||   : || ::|||| |::|
Db         66 FLINLAVSDLLLCITAVPITPVLAFMKRWIFGIIMCKLVPTCQAFSVLISSWSLCYIAID 125

Qy        153 KFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDGSFYVQPGET------ 206
              ::  |  | ::| | | |  :    |:|: | : |           :| |  :|
Db        126 RYRSIVTPLREPWSDRHARWLLMFTWVVAFLASYPL----------YYSQNLKTMVIENV 175

Qy        207 PYCGHFCDEANWQSENSRKI-YGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQF 265
                || || | ||||:   |: | |:::::| ::|  ::::||  |||||  | ::
Db        176 TLCGDFCGEFNWQSDEISKLTYTTSLLIIQLIIPAIIMSFCYLMILQKVQTDWLVDEGSM 235

Qy        266 CQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEW-------- 317
                ||  |::    ||::| |:|| ||: |: || ||: :|| :|     |:
Db        236 ---LTAAQQAQTAVRKRRVMYVLILMVIVFMACWFPLSAVNLFRDLGMRFEFCQTVYKVL 292

Qy        318 LKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRS 354
              :  | :|  :| ||||||: :||||:|:||:::: :|:
Db        293 MMDQMYFKLLNVHVIAMTSIVWNPVLYFWMSKRHRRA 329
```

RESULT 2
T19340
hypothetical protein C16D6.2 - Caenorhabditis elegans

```
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19340
R;Gardner, A.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19111
A;Accession: T19340
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-374 <WIL>
A;Cross-references: UNIPROT:O62062; UNIPARC:UPI00000806E6; EMBL:Z81472; PIDN:CAB03888.1;
A;Experimental source: clone C16D6
C;Genetics:
A;Gene: CESP:C16D6.2
A;Map position: X
A;Introns: 23/3; 56/2; 107/3; 147/3; 267/2; 306/3
C;Superfamily: neurokinin 1 receptor

  Query Match             24.8%;  Score 514;  DB 2;  Length 374;
  Best Local Similarity   31.3%;  Pred. No. 4.5e-36;
  Matches  114;  Conservative   74;  Mismatches  128;  Indels   48;  Gaps    9;

Qy         29 NNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQS 88
              |    |: :    :     :|::  :||  :| |||  :   || ||  |: |: |: ||| ||:
Db          2 NGSDCLNLNSELWLYR-EDLSSRWYIMLVFAFLYLIIIAAGIIGNSCVILAITRNKSLQT 60

Qy         89 ARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTA 148
                |:|:|:|  :|:::  |:  :||  |  |:| ||  :| : |      |:  ::::|||
Db         61 VPNLFILSLSCSDIVVCCTSATITPITAFKKEWIFGEALCRIAPFIAGISLCFSTFTLTA 120

Qy        149 ISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDGSFYVQPGETPY 208
              ||:|::: |  | ::|::  ||: :  :|   :  |  | :  |:   | |         :
Db        121 ISIDRYILIRFPMRKPITHYQAVGVIAIICAFAATITSPIM--FKQKLGEF------ENF 172

Qy        209 CGHFCDEANW-QSENSRKIYGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQFCQ 267
              || :| | ||  :|: |||||  :| || |:|: :|   |  |  |: : ||:: |
Db        173 CGQYCTE-NWGANESQRKIYGAALMFLQLVIPLTIIIISYTAISLKIGQSMILKGA---- 227

Qy        268 SLTQKQRSD------------ATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEP 315
                :||::|             |  |::: | :|| ||| |   |:     |:::|::  |
Db        228 ---KKQKTDNWEMELSDQQRIAVKRRQRTNRMLIGMVVAFACSWIWSVTFNILRDYEYLP 284

Qy        316 EWLKRQPFFWAINAHVIAMSLVVWNPLLF----------------FWLTRKQKRSG--LS 357
              | :| | : : |  | |||:  ||||||:                ||| |    |   |
Db        285 ELIKTQEYIFGIATHCIAMTSTVWNPLLYAVLNLQLRAAFIDLMPHWLRRHLNLEGDNSS 344

Qy        358 KILN 361
                :||
Db        345 PLLN 348


RESULT 3
T29741
hypothetical protein C39E6.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29741
R;Fulton, B.; Le, T.
submitted to the EMBL Data Library, February 1996
A;Description: The sequence of C. elegans cosmid C39E6.
A;Reference number: Z20676
A;Accession: T29741
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-457 <FUL>
A;Cross-references: UNIPROT:Q18534; UNIPARC:UPI000003C143; EMBL:U49944; PIDN:AAA93419.1;
C;Genetics:
A;Gene: CESP:C39E6.6
A;Introns: 58/3; 107/1; 169/3; 253/3; 274/2; 329/2; 366/2; 438/2
C;Superfamily: neurokinin 1 receptor

  Query Match             23.4%;  Score 485.5;  DB 2;  Length 457;
  Best Local Similarity   30.8%;  Pred. No. 1.5e-33;
  Matches  117;  Conservative   69;  Mismatches  117;  Indels   77;  Gaps   10;

Qy         58 FTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAM 117
              |  :| ||| ||:|||  :::    :| | | :|:|:|||  :| ::   ::|:||   :
Db         29 FLTVYLFLFFLGLFGNVTLIYVTCSHKALLSVQNIFILNLAASDCMMCILSLPITPITNV 88

Qy        118 TKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLI 177
               |:| ||:::|||:|      |:|| ::|| ||:||::: :   |    |:| | |   | |:
Db         89 YKNWYFGNLLCHLIPCIQGISIFVCTFSLGAIALDRYILVVRPHSTPLSQRGAFLTTVLL 148

Qy        178 WIVSTLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFV 237
              ||:| :: |||  : : :: :      |   ||:|| |  |:|  ||: |   ||| |||
Db        149 WILSFVVTLPYAFNMQMIEYT------EERICGYFCTE-KWESAKSRRAYTMIVMLAQFV 201

Qy        238 VPMAVITYCYFKILQKVSK-------DMIIQNA--------------QFCQSLT------ 270
              || ||: :||  |:  :||         |: : :                |:  |
Db        202 VPFAVMAFCYANIVSVLSKRAQTKIRKMVERTSALESSCAFPSHGLEQYENELNEFLDKQ 261

Qy        271 QKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEWLKRQPFF------ 324
              :|::     : ::   ||: |||  |   |||  :::|: ::          | ||
Db        262 EKEKQRVVLQNRRTTSILVTMVVWFGITWLPHNVISLIIEYD------DTQSFFRLYGRD 315

Qy        325 -----WAIN--AHVIAMSLVVWNPLLFFWL----------TRKQKRSGLSKILNST---- 363
                    : :|   | ||||  | ||:|: ||          |   |    :|:| |
Db        316 DYDISYLLNLFTHSIAMSNNVLNPVLYAWLNPSFRQLVIKTYFGDRRKSDRIINQTSVYK 375

Qy        364 ----------EGSKKAGGSG 373
                       |  | ||| |
Db        376 TKIVHDTKHLNGRAKIGGGG 395


RESULT 4
T20184
hypothetical protein C53C7.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20184
R;Mortimore, B.
submitted to the EMBL Data Library, November 1997
A;Reference number: Z19234
A;Accession: T20184
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-365 <WIL>
A;Cross-references: UNIPROT:Q9XXU4; UNIPARC:UPI000003C148; EMBL:AL008868; PIDN:CAA15513.
A;Experimental source: clone C53C7
C;Genetics:
A;Gene: CESP:C53C7.1
A;Map position: X
A;Introns: 40/2; 108/3; 136/2; 193/1; 254/3; 298/2; 336/3
C;Superfamily: neurokinin 1 receptor

  Query Match             22.3%;  Score 461.5;  DB 2;  Length 365;
  Best Local Similarity   30.9%;  Pred. No. 1.3e-31;
  Matches  110;  Conservative   79;  Mismatches  138;  Indels   29;  Gaps    8;

Qy         28 SNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQ 87
              |::  || |  |    |   |:|:     :|   :|  : |:|: ||  |: :| | | ||
Db          2 SSSNHCIDI-RAYLWQTKHDLTLHPIPIAILATIYTIIVVVGVTGNLLVVMSVMRFKVLQ 60

Qy         88 SARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLT 147
              | ||:|:::|  :|: :   :  |||  | :| | ||  :|||:||    ::  :: :||
Db         61 SVRNMFIVSLSVSDIFVAIVSGSVTPITAFSKVWLFGGPLCHLLPLLQGTALSFSTLTLT 120

Qy        148 AISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPY-----LMSFEHVDGSFYVQ 202
              ||::|::: |  |||:|:   |||  :      :|  :::|      || | :
Db        121 AIAIDRYILICHPTKEPIRKDQALKMISFNSAISVGLSVPLFMKQELMQFRN-------- 172

Qy        203 PGETPYCGHFCDEANWQSE-NSRKIYGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQ 261
                   ||| :| | ||  :   | :||| | ::||| |:  ||:||  |  |: : : ::
Db        173 -----YCGEYCSE-NWGPDAYLRSVYGTVVFIIQFVFPLITITFCYASISIKLRRGVFVR 226

Qy        262 NAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEWLKRQ 321
```

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Db        227 GSQ--KELMSEARRQLTQRRLRTNRMLIIMTVTFALSWLPSVGFNFLRDYSALPGIIDSQ 284

Qy        322 PFFWAINAHVIAMSLVVWNPLLFPWLTRKQKRSGLSKILNSTEGSKKAGGSGLRGI 377

Db        285 DYLFGIIFHCISMTSVIVNPFLYGY-CNEHFRAAFAALLDTVKAA-----CGMRRV 334


RESULT 5
T22076
hypothetical protein F41E7.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22076
R;Lennard, N.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z19509
A;Accession: T22076
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-412 <WIL>
A;Cross-references: UNIPROT:Q20275; UNIPARC:UPI000017663A; EMBL:Z68106; PIDN:CAA92126.1;
A;Experimental source: clone F41E7
C;Genetics:
A;Gene: CESP:F41E7.3
A;Map position: X
A;Introns: 76/2; 161/3; 220/3; 279/2; 325/2; 350/1; 378/1
C;Superfamily: neurokinin 1 receptor

  Query Match             20.2%;  Score 419.5;  DB 2;  Length 412;
  Best Local Similarity   29.4%;  Pred. No. 5.6e-28;
  Matches  101;  Conservative   72;  Mismatches   94;  Indels   77;  Gaps   13;

Qy         53 YIRSIFTFLYGFLFVLGIFGN----------------GGVLWAVARNKRLQSARNVFLL 95

Db          5 YFRPFFISMYCAVFLVASSGNFLVSNIIFDFSSFPTTVFKVVYVVMTNKRMQTITNIFIT 64

Qy         96 NLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPL----------------SN--S 136

Db         65 NLAVSDIMVNFTSLWLTPTYTSIGHWIFGGGLCHGLPLFQGIGLHIDGKLSSDQASNYTG 124

Qy        137 CSVFVTSWSLTAISLDKF---------LHINDPTKQPVSIRQALAITFLIWIVSTLINLP 187

Db        125 TSIFISTWTLTAIAIDRYIVIVHNSSNININD----RMSMRSCLSFIVLIWLCSLLLVTP 180

Qy        188 YL----MSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVI 243

Db        181 YAINMKLNYIHEPCDFLI----------CSE-DWSNAEFRSIFGIVVMILQFILPFVLI 228

Qy        244 TYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLT 303

Db        229 AISYIKI-------WLFLNSR--QSMTER-KSD-IKRKKRLLRMLIVMVVIFAICWFPFN 277

Qy        304 LLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWL 347

Db        278 LLNCLRDLKLD-NFMRGYFSFVFLSVHLMSMTATAWNPILYAFM 320


RESULT 6
T24487
hypothetical protein T05A1.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24487
R;Lloyd, C.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z19897
A;Accession: T24487
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-373 <WIL>
A;Cross-references: UNIPROT:Q22188; UNIPARC:UPI00001641C3; EMBL:Z68219; PIDN:CAA92481.1;
A;Experimental source: clone T05A1
C;Genetics:
A;Gene: CESP:T05A1.1
A;Map position: 4
A;Introns: 48/2; 106/3; 219/2; 254/1; 280/1; 309/1; 327/2

  Query Match             18.7%;  Score 387.5;  DB 2;  Length 373;
  Best Local Similarity   30.6%;  Pred. No. 2.6e-25;
  Matches   89;  Conservative   69;  Mismatches   98;  Indels   35;  Gaps    8;

Qy         47 DITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVF 106

Db         18 DMTNEPTVLVTFSLLYLHIFLLGILGNSAVLYLTMKHRQLQTVQNIFILNLCASNVLMCL 77

Qy        107 TAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVS 166

Db         78 TSLPITPITNVYKQWFFSSPVCKLIPLVQGASIFVSTFSLSAIALDRYNLVVRPHKQKLS 137

Qy        167 IRQALAITFLIWIVSTLINLPY--LMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSR 224

Db        138 SRSAMMIALLIWVISVVVCMPYGWYMDVEKLNG----------LCGEYCSE-HWPLAEVR 186

Qy        225 KIYGTTVMLLQFVVPMAVITYCYFKI----------LQKVS-KDMIIQNAQFCQSLTQK 272

Db        187 KGYTFLVLITQFLFPFATMAFCYYNIFSRLRQRVETKLKKLSERSQLLENSTTCGTTNHI 246

Qy        273 QRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNL--VKDFKKEPEWLKRQ 321

Db        247 VSINAVSK----GHIVYQGNNTF----LEITFLNVFFVLMYGSSSKWSGKQ 289


RESULT 7
T19186
hypothetical protein C10C6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19186
R;White, S.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z19086
A;Accession: T19186
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-376 <WIL>
A;Cross-references: UNIPROT:P90745; UNIPARC:UPI000003C14C; EMBL:Z83217; PIDN:CAB05681.1
A;Experimental source: clone C10C6
C;Genetics:
A;Gene: CESP:C10C6.2
A;Map position: 4
A;Introns: 54/3; 105/3; 133/3; 179/2; 251/2; 348/3
C;Superfamily: neurokinin 1 receptor

  Query Match             18.4%;  Score 382;  DB 2;  Length 376;
  Best Local Similarity   28.7%;  Pred. No. 7.8e-25;
  Matches   92;  Conservative   78;  Mismatches  127;  Indels   24;  Gaps    9;

Qy         54 IRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTP 113

Db         24 IRAIFSLLYLLVWVGAIVGNTLVLYVLTFNQVSLSVRTVFVGCLAGSDLLMCLFSLPITA 83

Qy        114 WYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAI 173

Db         84 ISIFSRVWVFPAIFCKLIGVFQGGTIFVSSFTLTVIALDRCVLILRPNQEIVNFPRAVFI 143

Qy        174 TFLIWIVSTLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENS-------RKI 226

Db        144 VFCIWLLGYSLALPVGI---YSDIAVYDE-----ICGTFCEE-NWPDFNPDTGRSGIRRA 194

Qy        227 YGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNY 286

Db        195 YGLSVLVLQFGIPALISSICYW-MISRVMSDQLARRRG--HNIRPESETKLVNRKTRANR 251

Qy        287 ILIAMVVTFIGCWLPLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFW 346
```

```
Db        252 MMIVMVVGFVLAWMPFNAVNLYRDLFGISKWYST---VFAL-CHVCAMCSAVLNPIIYSW 307

Qy        347 LTRKQKRSGLSKILNSTEGSK 367
                | |  :: :   |: ::
Db        308 F-NPQFRQSITTLFKGTDEAR 327


RESULT 8
I52315
G protein-coupled receptor UHR-1 - rat
C;Species: Rattus sp. (rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-May-2000
C;Accession: I52315
R;Welch, S.K.; O'Hara, B.F.; Kilduff, T.S.; Heller, H.C.
Biochem. Biophys. Res. Commun. 209, 606-613, 1995
A;Title: Sequence and tissue distribution of a candidate G-coupled receptor cloned from
A;Reference number: I52315; MUID:95251659; PMID:7733930
A;Accession: I52315
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-370 <RES>
A;Cross-references: UNIPARC:UPI000004B9B3; GB:S77867; NID:g998527; PIDN:AAB34129.1; PID:
C;Superfamily: neurokinin 1 receptor

  Query Match             18.0%;  Score 373.5;  DB 1;  Length 370;
  Best Local Similarity   26.7%;  Pred. No. 4.1e-24;
  Matches   93;  Conservative   80;  Mismatches  154;  Indels   21;  Gaps    8;

Qy         18 STISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVL 77
              || :|     | :     :  | |      : :   :: :   ||  : |:|: ||  ::
Db         23 STPANQSAEASESNVSATVPRAAAVTPFQSLQLVHQLKGLIVMLYSIVVVVGLVGNCLLV 82

Qy         78 WAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAM-TKDWAFGSVMCHLVPLSNS 136
                :|| :|| :  |  : ||  :|:::    :|:|  ||   : | ||  :||||
Db         83 LVIARVRRLHNVTNFLIGNLALSDVLMCAACVPLTLAYAFEPRGWVFGGGLCHLVFFLQP 142

Qy        137 CSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVD 196
              :|:|: ::|| |::|::: :  | :: :|:: :      || :| :: ||  :   ||:
Db        143 VTVYVSVFTLTTIAVDRYVVLVHPLRRRISLKLSAYAVLGIWALSAVLALPAAVHTYHVE 202

Qy        197 GSFYVQPGETPYCGHFCDEANWQS-ENSRKIYGTTVMLLQFVVPMAVITYCYFKILQKVS 255
                ::| :   |  |      | | |  |:||   ::|  :::|:  |    | ::  |
Db        203 ----LKPHDVRLCEEF-----WGSQERQRQIYAWGLLLGTYLLPLLAILLSYVRVSVK-- 251

Qy        256 KDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEP 315
                ::|      |:|| |     :|:::   :|: :|| |  ||||| : ||::|   :|
Db        252 ----LRNRVVPGSVTQSQADWDRARRRRTFCLLVVVVVVFALCWLPLHIFNLLRDL--DP 305

Qy        316 EWLKRQPF-FWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKILNS 362
                :   |   :  | :|||   :|| :: ||      |  | |:| |
Db        306 RAIDPYAFGLVQLLCHWLAMSSACYNPFIYAWL-HDSFREELRKMLLS 352


RESULT 9
S63685
neuropeptide Y receptor D type - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S63685
R;Gregor, P.; Millham, M.L.; Feng, Y.; DeCarr, L.B.; McCaleb, M.L.; Cornfield, L.J.
FEBS Lett. 381, 58-62, 1996
A;Title: Cloning and characterization of a novel receptor to pancreatic polypeptide, a m
A;Reference number: S63685; MUID:96193913; PMID:8641440
A;Accession: S63685
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-375 <GRE>
A;Cross-references: UNIPROT:Q61041; UNIPARC:UPI0000027CC7; EMBL:U40189; NID:g1223969; PI
C;Superfamily: neurokinin 1 receptor

  Query Match             17.1%;  Score 354;  DB 2;  Length 375;
  Best Local Similarity   25.7%;  Pred. No. 1.9e-22;
  Matches  103;  Conservative   74;  Mismatches  142;  Indels   82;  Gaps   12;

Qy         21 SNVITSHSN-NGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWA 79
              :| : |  | :  |  || :|          | | :     |    :||: ||  :::
Db         21 TNPLDSPYNFSDGCQDSAELLA----------FIITT-----YSIETILGVLGNLCLIFV 65

Qy         80 VARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSV 139
              | |   :  |: : || |:| ::      |:|  | :   | || |:| ::      ||
Db         66 TTRQKEKSNVTNLLIANLAFSDFLMCLICQPLTVTYTIMDYWIFGEVLCKMLTFIQCMSV 125

Qy        140 FVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMS-----FEH 194
              |:  ||  ::|::   | :||    || ||      :|| :|  ::||:| :       |
Db        126 TVSILSLVLVALERHQLIINPTGWKPSIFQAYLGIVVIWFISCFLSLPFLANSTLNDLFH 185

Qy        195 VDGSFYVQPGETPYCGHFCDE-----ANWQSENSRKIYGTTVMLLQFVVPMAVITYCYFK 249
              : |  |:         | ::      :| |:: | || | ::| |: :|:| |  || :
Db        186 YNHSKVVE---------FLEDKVVCFVSWSSDHHRLIYTTFLLLFQYCIPLAFILVCYIR 236

Qy        250 ILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVK 309
              | |:: :   : :|  |         |    : |::| :|: ||  |   ||| : | ::
Db        237 IYQRLQRQKHVFHAHAC--------SSRAGQMKRINSMLMTMVTAFAVLWLPLHVFNTLE 288

Qy        310 DFKKEPEWLKRQPFFWAINA----------HVIAMSLVVWNPLLFFWLTRKQKRSGLSKI 359
              |: :|              || |          |::||:    || :: :|    |:   : :
Db        289 DWYQE-----------AIPACHGNLIFLMCHLLAMASTCVNPFIYGFLNINFKKDIKALV 337

Qy        360 L----NSTEGSKKAGGSGLRGIQLHDLLPTST-HSDRCAGN 395
              |    | :|             : || || |:|   |:
Db        338 LTCHCRSPQGES-------------EHLPLSTVHTDLSKGS 365


RESULT 10
A45490
neuropeptide Y/peptide YY receptor Y1 - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A45490; A46133; A42773
R;Herzog, H.; Baumgartner, M.; Vivero, C.; Selbie, L.A.; Auer, B.; Shine, J.
J. Biol. Chem. 268, 6703-6707, 1993
A;Title: Genomic organization, localization, and allelic differences in the gene for the
A;Reference number: A45490; MUID:93203272; PMID:8095935
A;Accession: A45490
A;Molecule type: DNA
A;Residues: 1-384 <HER>
A;Cross-references: UNIPROT:P25929; UNIPARC:UPI000002D509; GB:L07615; NID:g189284; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBIN:128005, NCBIP:128000)
R;Herzog, H.; Hort, Y.J.; Ball, H.J.; Hayes, G.; Shine, J.; Selbie, L.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992
A;Title: Cloned human neuropeptide Y receptor couples to two different second messenger
A;Reference number: A46133; MUID:92335184; PMID:1321422
A;Accession: A46133
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-384 <HE2>
A;Cross-references: UNIPARC:UPI000002D509
A;Note: sequence extracted from NCBI backbone (NCBIP:108538)
R;Larhammar, D.; Blomqvist, A.G.; Yee, F.; Jazin, E.; Yoo, H.; Wahlested, C.
J. Biol. Chem. 267, 10935-10938, 1992
A;Title: Cloning and functional expression of a human neuropeptide Y/peptide YY receptor
A;Reference number: A42773; MUID:92283782; PMID:1317848
A;Accession: A42773
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-384 <LAR>
A;Cross-references: UNIPARC:UPI000002D509; GB:M88461; NID:g189155; PIDN:AAA73215.1; PID.
A;Experimental source: fetal brain
A;Note: sequence extracted from NCBI backbone (NCBIN:104735, NCBIP:104736)
C;Genetics:
A;Gene: GDB:NPY1R; NPYR
A;Cross-references: GDB:132643; OMIM:162641
A;Map position: 4q31.3-4q32
C;Superfamily: neurokinin 1 receptor
C;Keywords: appetite; G protein-coupled receptor; glycoprotein; lipoprotein; thiolester
F;37-66/Domain: transmembrane #status predicted <TM1>
```

```
F;77-103/Domain: transmembrane #status predicted <TM2>
F;118-136/Domain: transmembrane #status predicted <TM3>
F;155-179/Domain: transmembrane #status predicted <TM4>
F;209-232/Domain: transmembrane #status predicted <TM5>
F;261-286/Domain: transmembrane #status predicted <TM6>
F;300-323/Domain: transmembrane #status predicted <TM7>
F;113-198/Disulfide bonds: #status predicted
F;186/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;338/Binding site: palmitate (Cys) (covalent) #status predicted

  Query Match             16.7%;  Score 346.5;  DB 2;  Length 384;
  Best Local Similarity   25.7%;  Pred. No. 8.4e-22;
  Matches   88;  Conservative   78;  Mismatches  154;  Indels   23;  Gaps    6;

Qy         18 STISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVL 77
              ||: : : :|| : :  :    : |   ||  :   :       || : :||: ||  ::
Db          3 STLFSQVENHSVHSNFSEKNAQLLAFENDDCHLPLAMIFTLALAYGAVIILGVSGNLALI 62

Qy         78 WAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSC 137
               : : | :::  |: ::|| |:||::    :| |  | :   | ||  || | |
Db         63 IIILKQKEMRNVTNILIVNLSFSDLLVAIMCLPFTFVYTLMDHWVFGEAMCKLNPFVQCV 122

Qy        138 SVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLM------- 190
              |: |: :||  |:::   | :|     : | |     :||:::   :||:|:
Db        123 SITVSIFSLVLIAVERHQLIINPRGWRPNNRHAYVGIAVIWVLAVASSLPFLIYQVMTDE 182

Qy        191 SFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYCYFKI 250
              |::|    |          : | :  : |:: |  | | :::||:  |:  |  |||||
Db        183 PFQNVTLDAYKDK-------YVCFD-QFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKI 234

Qy        251 LQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKD 310
               :: :   :|    :    | ||  |   |::| :|:::|| |  ||||||: | | |
Db        235 YIRLKR----RNNMMDKMRDNKYRSSET---KRINIMLLSIVVAFAVCWLPLTIFNTVFD 287

Qy        311 FKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKR 353
              :  :         : :  |: ||     ||: : :| :  :|
Db        288 WNHQIIATCNHNLLFLL-CHLTAMISTCVNPIFYGFLNKNFQR 329


RESULT 11
S27388
neuropeptide Y receptor NPY-1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S27388
R;Eva, C.; Oberto, A.; Sprengel, R.; Genazzani, E.
FEBS Lett. 314, 285-288, 1992
A;Title: The murine NPY-1 receptor gene. Structure and delineation of tissue-specific ex
A;Reference number: S27388; MUID:93106169; PMID:1468559
A;Accession: S27388
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-382 <EVA>
A;Cross-references: UNIPROT:Q04573; UNIPARC:UPI0000024A23; EMBL:Z18280; NID:g53438; PIDN
C;Superfamily: neurokinin 1 receptor

  Query Match             16.5%;  Score 342;  DB 2;  Length 382;
  Best Local Similarity   25.6%;  Pred. No. 2e-21;
  Matches   87;  Conservative   80;  Mismatches  155;  Indels   18;  Gaps    6;

Qy         18 STISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVL 77
              ||: : : :|| : :  :  :  :| :  ||  :   :       || : :||: ||  ::
Db          3 STLFSKVENHSIHYNASENSPLLAFEN-DDCHLPLAVIFTLALAYGAVIILGVSGNLALI 61

Qy         78 WAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSC 137
               : : | :::  |: ::|| |:||::    :| |  | :   | ||  || | |
Db         62 IIILKQKEMRNVTNILIVNLSFSDLLVAVMCLPFTFVYTLMDHWVFGETMCKLNPFVQCV 121

Qy        138 SVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDG 197
              |: |: :||  |::::   | :|     : | |     :||:::   :||:::     |
Db        122 SITVSIFSLVLIAVERHQLIINPRGWRPNNRHAYIGITVIWVLAVASSLPFVIYQILTD- 180

Qy        198 SFYVQPGETPYCGHFCDE----ANWQSENSRKIYGTTVMLLQFVVPMAVITYCYFKILQK 253
                :| :      | |:      : |:: |  | | :::||:  |:  |  |||||  :
Db        181 ----EPFQNVSLAAFKDKYVCFDKFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIR 236

Qy        254 VSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKK 313
              : :    :|    :    | ||  |   |::| :|:::|| |  ||||||: | | |:
Db        237 LKR----RNNMMDKIRDSKYRSSET---KRINIMLLSIVVAFAVCWLPLTIFNTVFDWNH 289

Qy        314 EPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKR 353
              :          : :  |: ||     ||: : :| :  :|
Db        290 QIIATCNHNLLFLL-CHLTAMISTCVNPIFYGFLNKNFQR 328


RESULT 12
A41738
neuropeptide Y receptor - fruit fly (Drosophila melanogaster)
N;Alternate names: G protein-coupled receptor PR4
C;Species: Drosophila melanogaster
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C;Accession: A41738
R;Li, X.J.; Wu, Y.N.; North, R.A.; Forte, M.
J. Biol. Chem. 267, 9-12, 1992
A;Title: Cloning, functional expression, and developmental regulation of a neuropeptide
A;Reference number: A41738; MUID:92112730; PMID:1370455
A;Accession: A41738
A;Molecule type: mRNA
A;Residues: 1-449 <LIA>
A;Cross-references: UNIPROT:P25931; UNIPARC:UPI0000130B36; GB:M81490; NID:g157996; PIDN
C;Genetics:
A;Gene: FlyBase:NepYr
A;Cross-references: FlyBase:FBgn0004842
C;Superfamily: neurokinin 1 receptor
C;Keywords: appetite; G protein-coupled receptor; transmembrane protein

  Query Match             16.2%;  Score 337;  DB 2;  Length 449;
  Best Local Similarity   27.0%;  Pred. No. 6.5e-21;
  Matches   88;  Conservative   75;  Mismatches  145;  Indels   18;  Gaps   10;

Qy         46 DDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILV 105
              :|:    | : |   ||  :|:  : ||| | : |     |:::  | |: :|   |:::
Db         81 EDMWSSAYFKIIVYMLYIPIFIFALIGNGTVCYIVYSTPRMRTVTNYFIASLAIGDILMS 140

Qy        106 FTAIPVTPWYAM--TKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQ 163
              |   | : : ::     | ||  :|| |   | : || |::::| |||:|::: |  | |
Db        141 FFCEP-SSFISLFILNYWPFGLALCHFVNYSQAVSVLVSAYTLVAISIDRYIAIMWPLKP 199

Qy        164 PVSIRQALAITFLIWIVSTLINLPYLMSFEHVDG-SFYVQPGETPYCGHFCDEANWQSEN 222
              :: | |   |  :| ::    ||  :    | |   :  | |    : | |  | | :
Db        200 RITKRYATFIIAGVWFIALATALPIPI----VSGLDIPMSPWHTKCEKYICREM-WPSRS 254

Qy        223 SRKIYGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKK 282
              |  ::  ||||||: |: : | :|  :|         |:     | : :  | |::|
Db        255 QEYYYTLSLFALQFVVPLGVLIFTYARITIRVWAKRPPGEAE-----TNRDQRMARSKRK 309

Qy        283 KVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPL 342
              |  ::: :|: |  ||||  :| |: : ::   |     |: |     | :|||   :||:
Db        310 MVK-MMLTVVIVFTCCWLPFNILQLLLNDEEFAHW-DPLPYVW-FAFHWLAMSHCCYNPI 366

Qy        343 LFFWLTRKQKRSGLSKILNSTEGSKK 368
              :: ::  :  |||  ::::   | ::
Db        367 IYCYMNAR-FRSGFVQLMHRMPGLRR 391


RESULT 13
S12863
G protein-coupled receptor FC5 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: S12863; S19101
R;Eva, C.; Keinaenen, K.; Monyer, H.; Seeburg, P.; Sprengel, R.
FEBS Lett. 271, 81-84, 1990
A;Title: Molecular cloning of a novel G protein-coupled receptor that may belong to the
A;Reference number: S12863; MUID:91032093; PMID:2172008
A;Accession: S12863
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A;Molecule type: mRNA
A;Residues: 1-349 <EVA>
A;Cross-references: UNIPROT:P21555; UNIPARC:UPI0000176632; EMBL:Z11504
R;Krause, J.; Eva, C.; Seeburg, P.; Sprengel, R.
submitted to the EMBL Data Library, November 1991
A;Description: Pharmacological and Transduction Properties of a Recombinantly Expressed
A;Reference number: S19101
A;Accession: S19101
A;Molecule type: mRNA
A;Residues: 1-343,'DDYETIAMSTMHTDVSKTSLKQASPVAFKKISMNDNEKI' <KRA>
A;Cross-references: UNIPARC:UPI0000130B23; EMBL:Z11504; NID:g57636; PIDN:CAA77579.1; PID
C;Superfamily: neurokinin 1 receptor
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F;39-61/Domain: transmembrane #status predicted <TM1>
F;73-93/Domain: transmembrane #status predicted <TM2>
F;114-135/Domain: transmembrane #status predicted <TM3>
F;155-175/Domain: transmembrane #status predicted <TM4>
F;213-231/Domain: transmembrane #status predicted <TM5>
F;262-285/Domain: transmembrane #status predicted <TM6>
F;299-322/Domain: transmembrane #status predicted <TM7>
F;2,11,17/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;346/Binding site: phosphate (Thr) (covalent) #status predicted

  Query Match             16.1%;  Score 333;  DB 2;  Length 349;
  Best Local Similarity   25.3%;  Pred. No. 1.1e-20;
  Matches   86;  Conservative   81;  Mismatches  155;  Indels   18;  Gaps    6;

Qy         18 STISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVL 77
Db          3 STLFSRVENYSVHYNVSENSPFLAFEN-DDCHLPLAVIFTLALAYGAVIILGVSGNLALI 61

Qy         78 WAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSC 137
Db         62 IIILKQKEMRNVTNILIVNLSFSDLLVAVMCLPFTFVYTLMDHWVFGETMCKLNPFVQCV 121

Qy        138 SVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDG 197
Db        122 SITVSIFSLVLIAVERHQLIINPRGWRPNNRHAYIGITVIWVLAVASSLPFVIYQILTD- 180

Qy        198 SFYVQPGETPYCGHFCDE----ANWQSENSRKIYGTTVMLLQFVVPMAVITYCYFKILQK 253
Db        181 ----EPFQNVSLAAFKDKYVCFDKFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIR 236

Qy        254 VSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKK 313
Db        237 LKR----RNNMMDKIRDSKYRSSET---KRINVMLLSIVVAFAVCWLPLTIFNTVFDWNH 289

Qy        314 EPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKR 353
Db        290 QIIATCNHNLLFLL-CHLTAMISTCVNPIFYGFLNKNFQR 328


RESULT 14
B46133
neuropeptide Y/peptide YY receptor Y1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000
C;Accession: B46133
R;Herzog, H.; Hort, Y.J.; Ball, H.J.; Hayes, G.; Shine, J.; Selbie, L.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992
A;Title: Cloned human neuropeptide Y receptor couples to two different second messenger
A;Reference number: A46133; MUID:92335184; PMID:1321422
A;Accession: B46133
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-382 <HER>
A;Cross-references: UNIPARC:UPI0000130B23
A;Note: sequence extracted from NCBI backbone (NCBIP:108539)
C;Superfamily: neurokinin 1 receptor
C;Keywords: appetite; G protein-coupled receptor; transmembrane protein

  Query Match             16.1%;  Score 333;  DB 2;  Length 382;
  Best Local Similarity   25.3%;  Pred. No. 1.2e-20;
  Matches   86;  Conservative   81;  Mismatches  155;  Indels   18;  Gaps    6;

Qy         18 STISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVL 77
Db          3 STLFSRVENYSVHYNVSENSPFLAFEN-DDCHLPLAVIFTLALAYGAVIILGVSGNLALI 61

Qy         78 WAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSC 137
Db         62 IIILKQKEMRNVTNILIVNLSFSDLLVAVMCLPFTFVYTLMDHWVFGETMCKLNPFVQCV 121

Qy        138 SVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDG 197
Db        122 SITVSIFSLVLIAVERHQLIINPRGWRPNNRHAYIGITVIWVLAVASSLPFVIYQILTD- 180

Qy        198 SFYVQPGETPYCGHFCDE----ANWQSENSRKIYGTTVMLLQFVVPMAVITYCYFKILQK 253
Db        181 ----EPFQNVSLAAFKDKYVCFDKFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKIYIR 236

Qy        254 VSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKK 313
Db        237 LKR----RNNMMDKIRDSKYRSSET---KRINVMLLSIVVAFAVCWLPLTIFNTVFDWNH 289

Qy        314 EPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKR 353
Db        290 QIIATCNHNLLFLL-CHLTAMISTCVNPIFYGFLNKNFQR 328


RESULT 15
I39187
neuropeptide Y/peptide YY receptor Y2 - human
N;Alternate names: neuropeptide y/peptide YY receptor type 2
C;Species: Homo sapiens (man)
C;Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: I39187; I39163; G02301
R;Gerald, C.; Walker, M.W.; Vaysse, P.J.
J. Biol. Chem. 270, 26758-26761, 1995
A;Title: Expression cloning and pharmacological characterization of a human hippocampal
A;Reference number: I39187; MUID:96070760; PMID:7592910
A;Accession: I39187
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-381 <GER>
A;Cross-references: UNIPROT:P49146; UNIPARC:UPI000003B342; EMBL:U36269; NID:g1063633; PI
R;Rose, P.M.; Fernandes, P.; Lynch, J.S.; Frazier, S.T.; Fisher, S.M.; Kodukula, K.; Kie
J. Biol. Chem. 270, 22661-22664, 1995
A;Title: Cloning and functional expression of a cDNA encoding a human type 2 neuropeptic
A;Reference number: I39163; MUID:96032678; PMID:7559383
A;Accession: I39163
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-133,'A',135-381 <ROS>
A;Cross-references: UNIPARC:UPI000016A22B; EMBL:U32500; NID:g1000750; PIDN:AAA93170.1; P
R;Yan, H.; Yang, J.; Marasco, J.; Yamaguchi, K.; Brenner, S.; Collins, F.; Karbon, W.
submitted to the EMBL Data Library, December 1995
A;Reference number: H01019
A;Accession: G02301
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-171,'G',173,'R',175-201,'P',203-208,'A',210-381 <YAN>
A;Cross-references: UNIPARC:UPI000016B18D; EMBL:U42389; NID:g1314329; PIDN:AAB07760.1; P
C;Genetics:
A;Gene: GDB:NPY2R
A;Cross-references: GDB:4365607; OMIM:162642
A;Map position: 4q31-4q31
C;Superfamily: neurokinin 1 receptor
C;Keywords: appetite; G protein-coupled receptor; glycoprotein; lipoprotein; thiolester
F;49-76/Domain: transmembrane #status predicted <TM1>
F;87-113/Domain: transmembrane #status predicted <TM2>
F;166-186/Domain: transmembrane #status predicted <TM4>
F;221-237/Domain: transmembrane #status predicted <TM5>
F;269-291/Domain: transmembrane #status predicted <TM6>
F;305-328/Domain: transmembrane #status predicted <TM7>
F;123-203/Disulfide bonds: #status predicted
```

```
F;342/Binding site: palmitate (Cys) (covalent) #status predicted
F;372/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             15.6%;  Score 324;  DB 2;  Length 381;
  Best Local Similarity   25.5%;  Pred. No. 6.9e-20;
  Matches   91;  Conservative   67;  Mismatches  139;  Indels   60;  Gaps    9;

Qy         37 AEAIAAQGIDDITVDFY-------------------------IRSIFTFLYGFLFVLGI 70
              |||    | :::: |: |                          :: :    |  : :||:
Db          6 AEADENQTVEEMKVEQYGPQTTPRGELVPDPEPELIDSTKLIEVQVVLILAYCSIILLGV 65

Qy         71 FGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHL 130
               ||  |:  | : | ::: | |: ||   ||::    :| |  | :  :|  | |:|||
Db         66 IGNSLVIHVVIKFKSMRTVTNFFIANLAVADLLVNTLCLPFTLTYTLMGEWKMGPVLCHL 125

Qy        131 VPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLM 190
              || :   :| |:: :|| |:||:   |    :  :| | :  |  | | :| |:  |  :
Db        126 VPYAQGLAVQVSTITLTVIALDRHRCIVYHLESKISKRISFLIIGLAWGISALLASPLAI 185

Qy        191 SFEH----VDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGT----TVMLLQFVVPMAV 242
                |:    :   | :           | |  |  |  : ||||    : :|: :|:|: :
Db        186 FREYSLIEIIPDFEIVA---------CTE-KWPGE-EKSIYGTVYSLSSLLILYVLPLGI 234

Qy        243 ITYCYFKILQKVSKDMI--IQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 300
              |:: | :|  |:   :     |  : |             |::|   :|: :|| |   ||
Db        235 ISFSYTRIWSKLKNHVSPGAANDHYHQ-----------RRQKTTKMLVCVVVVFAVSWL 282

Qy        301 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLS 357
              ||    |  |   :   ||     : :  |:|||     ||||: |:    ::: ||
Db        283 PLHAFQLAVDIDSQVLDLKEYKLIFTV-FHIIAMCSTFANPLLYGWMNSNYRKAFLS 338

Search completed: May  8, 2006, 09:34:15
Job time : 42 secs
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GenCore version 5.1.8

OM protein - protein search, using sw model

Run on: May 8, 2006, 09:26:17 ; Search time 187 Seconds
(without alignments)
932.799 Million cell updates/sec

Title: US-10-650-467-105
Perfect score: 2074
Sequence: 1 MVSSAATISTISTTTTPSTI.....QLHDLLPTSTHSDRCAGNSF 397

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2074	100.0	397	4	AAU03851	Aau03851 G protein
2	2074	100.0	499	4	AAU03820	Aau03820 G protein
3	1899	91.6	433	4	AAU03852	Aau03852 G protein
4	607.5	29.3	450	4	AAU03809	Aau03809 G protein
5	607.5	29.3	539	8	ADN23955	Adn23955 Bacterial
6	529	25.5	518	4	AAB86955	Aab86955 D. melano
7	529	25.5	600	4	ABB71560	Abb71560 Drosophil
8	529	25.5	600	4	AAU03205	Aau03205 Fruit fly
9	529	25.5	600	7	AAE38182	Aae38182 Fruit fly
10	529	25.5	600	7	ADL83372	Adl83372 Drosophil
11	529	25.5	600	8	ADR03092	Adr03092 Drosophil
12	529	25.5	600	9	ADV91972	Adv91972 DmGPCR1,
13	521	25.1	600	7	ADE14524	Ade14524 Fruit fly
14	515.5	24.9	376	4	AAU03811	Aau03811 G protein
15	514	24.8	374	8	ADN24291	Adn24291 Bacterial
16	485.5	23.4	457	4	AAU03813	Aau03813 G protein
17	485.5	23.4	457	8	ADN24116	Adn24116 Bacterial
18	461.5	22.3	365	4	AAU03818	Aau03818 G protein
19	461.5	22.3	365	8	ADN24305	Adn24305 Bacterial
20	460.5	22.2	387	4	AAU03808	Aau03808 G protein
21	458	22.1	381	4	AAU03807	Aau03807 G protein
22	458	22.1	402	4	AAU03805	Aau03805 G protein
23	458	22.1	404	4	AAU03804	Aau03804 G protein
24	458	22.1	406	4	AAU03806	Aau03806 G protein
25	419.5	20.2	412	8	ADN24230	Adn24230 Bacterial
26	390.5	18.8	375	6	ABG73520	Abg73520 D. rerio
27	388	18.7	458	4	AAU03207	Aau03207 Fruit fly
28	388	18.7	458	7	ADL83376	Adl83376 Drosophil
29	388	18.7	458	8	ADR03096	Adr03096 Drosophil
30	388	18.7	458	9	ADV91976	Adv91976 DmGPCR2b,
31	387.5	18.7	373	8	ADN23444	Adn23444 Bacterial
32	386.5	18.6	370	8	ADO29366	Ado29366 Mouse GPC
33	386.5	18.6	380	2	AAW27510	Aaw27510 Consensus
34	386	18.6	370	2	AAR91218	Aar91218 Human pit
35	386	18.6	370	2	AAW31379	Aaw31379 Human G p
36	386	18.6	370	2	AAW95181	Aaw95181 Human G-p
37	386	18.6	370	2	AAW97221	Aaw97221 Human pit
38	386	18.6	370	4	AAG62539	Aag62539 Human CRH
39	386	18.6	370	6	ABP81880	Abp81880 Human G p
40	386	18.6	370	8	ADO29365	Ado29365 Human GPC
41	386	18.6	370	8	ADT98602	Adt98602 Human wil
42	385.5	18.6	370	3	AAY87503	Aay87503 Murine G
43	385.5	18.6	370	4	AAB67653	Aab67653 Amino aci
44	382	18.4	370	3	AAY87505	Aay87505 Human G c
45	382	18.4	376	4	AAU03822	Aau03822 G protein

ALIGNMENTS

RESULT 1
AAU03851
ID AAU03851 standard; protein; 397 AA.
XX
AC AAU03851;
XX
DT 12-SEP-2001 (first entry)
XX
DE G protein-coupled receptor-like (GPCR-like) receptor protein #23.
XX
KW G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;
KW endoparasite; ectoparasite; invertebrate; insect; neurological disorder;
KW neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech;
KW fruitfly.
XX
OS Homo sapiens.
XX
PN WO200138533-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-US032225.
XX
PR 24-NOV-1999; 99US-0167523P.
XX
PA (PHAA) PHARMACIA & UPJOHN.
XX
PI Lowery DE, Geary TG, Kubiak TM, Larsen MJ;
XX
DR WPI; 2001-343952/36.
DR N-PSDB; AAS07253.
XX
PT Using G-protein-coupled receptor (GPCR)-like receptors to identify
PT candidate compounds for the treatment and prevention of invertebrate
PT parasites, especially helminths and insects.
XX
PS Claim 6; Page 175-176; 219pp; English.
XX
CC The sequence represents a G protein-coupled receptor-like (GPCR-like)
CC receptor protein. GPCR-like receptors and their associated nucleic acids
CC may be used to identify candidate compounds for their ability to modulate
CC the activity of GPCRs. The sequences therefore are useful for treating
CC and preventing infection by endoparasitic and ectoparasitic invertebrate
CC parasites, especially helminths and insects, and particularly ailments
CC related to aberrant neurological and neuromuscular function
XX
SQ Sequence 397 AA;

```
  Query Match             100.0%;  Score 2074;  DB 4;  Length 397;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-209;
  Matches  397;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MVSSAATISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MVSSAATISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF 60

Qy         61 LYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKD 120

Qy        121 WAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 WAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIV 180

Qy        181 STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM 240

Qy        241 AVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 300

Qy        301 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKIL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKIL 360

Qy        361 NSTEGSKKAGGSGLRGIQLHDLLPTSTHSDRCAGNSF 397
              |||||||||||||||||||||||||||||||||||||
Db        361 NSTEGSKKAGGSGLRGIQLHDLLPTSTHSDRCAGNSF 397
```

```
RESULT 2
AAU03820
ID   AAU03820 standard; protein; 499 AA.
XX
AC   AAU03820;
XX
DT   12-SEP-2001  (first entry)
XX
DE   G protein-coupled receptor-like (GPCR-like) receptor protein #19.
XX
KW   G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;
KW   endoparasite; ectoparasite; invertebrate; insect; neurological disorder;
KW   neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech;
KW   fruitfly.
XX
OS   Homo sapiens.
XX
PN   WO200138533-A2.
XX
PD   31-MAY-2001.
XX
PF   24-NOV-2000; 2000WO-US032225.
XX
PR   24-NOV-1999;   99US-0167523P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN.
XX
PI   Lowery DE,  Geary TG,  Kubiak TM,  Larsen MJ;
XX
DR   WPI; 2001-343952/36.
DR   N-PSDB; AAS07219.
XX
PT   Using G-protein-coupled receptor (GPCR)-like receptors to identify
PT   candidate compounds for the treatment and prevention of invertebrate
PT   parasites, especially helminths and insects.
XX
PS   Claim 6; Page 147-149; 219pp; English.
XX
CC   The sequence represents a G protein-coupled receptor-like (GPCR-like)
CC   receptor protein. GPCR-like receptors and their associated nucleic acids
CC   may be used to identify candidate compounds for their ability to modulate
CC   the activity of GPCRs. The sequences therefore are useful for treating
CC   and preventing infection by endoparasitic and ectoparasitic invertebrate
CC   parasites, especially helminths and insects, and particularly ailments
CC   related to aberrant neurological and neuromuscular function
XX
SQ   Sequence 499 AA;
```

```
  Query Match             100.0%;  Score 2074;  DB 4;  Length 499;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-209;
  Matches  397;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MVSSAATISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        103 MVSSAATISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF 162

Qy         61 LYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 LYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKD 222

Qy        121 WAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        223 WAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIV 282

Qy        181 STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM 342

Qy        241 AVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 AVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 402

Qy        301 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKIL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKIL 462

Qy        361 NSTEGSKKAGGSGLRGIQLHDLLPTSTHSDRCAGNSF 397
              |||||||||||||||||||||||||||||||||||||
Db        463 NSTEGSKKAGGSGLRGIQLHDLLPTSTHSDRCAGNSF 499
```

```
RESULT 3
AAU03852
ID   AAU03852 standard; protein; 433 AA.
XX
AC   AAU03852;
XX
DT   12-SEP-2001  (first entry)
XX
DE   G protein-coupled receptor-like (GPCR-like) receptor protein #24.
XX
KW   G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;
KW   endoparasite; ectoparasite; invertebrate; insect; neurological disorder;
KW   neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech;
KW   fruitfly.
XX
OS   Homo sapiens.
XX
PN   WO200138533-A2.
XX
PD   31-MAY-2001.
XX
PF   24-NOV-2000; 2000WO-US032225.
XX
PR   24-NOV-1999;   99US-0167523P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN.
XX
PI   Lowery DE,  Geary TG,  Kubiak TM,  Larsen MJ;
XX
DR   WPI; 2001-343952/36.
DR   N-PSDB; AAS07254.
```

XX
PT Using G-protein-coupled receptor (GPCR)-like receptors to identify
PT candidate compounds for the treatment and prevention of invertebrate
PT parasites, especially helminths and insects.
XX
PS Claim 6; Page 179-180; 219pp; English.
XX
CC The sequence represents a G protein-coupled receptor-like (GPCR-like)
CC receptor protein. GPCR-like receptors and their associated nucleic acids
CC may be used to identify candidate compounds for their ability to modulate
CC the activity of GPCRs. The sequences therefore are useful for treating
CC and preventing infection by endoparasitic and ectoparasitic invertebrate
CC parasites, especially helminths and insects, and particularly ailments
CC related to aberrant neurological and neuromuscular function
XX
SQ Sequence 433 AA;

Query Match 91.6%; Score 1899; DB 4; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.4e-190;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MVSSAATISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MVSSAATISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF 60

Qy         61 LYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKD 120

Qy        121 WAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 WAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIV 180

Qy        181 STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM 240

Qy        241 AVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 300

Qy        301 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKIL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKIL 360

Qy        361 NSTE 364
              ||||
Db        361 NSTE 364
```

RESULT 4
AAU03809
ID AAU03809 standard; protein; 450 AA.
XX
AC AAU03809;
XX
DT 12-SEP-2001 (first entry)
XX
DE G protein-coupled receptor-like (GPCR-like) receptor protein #8.
XX
KW G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;
KW endoparasite; ectoparasite; invertebrate; insect; neurological disorder;
KW neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech;
KW fruitfly.
XX
OS Homo sapiens.
XX
PN WO200138533-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-US032225.
XX
PR 24-NOV-1999; 99US-0167523P.
XX
PA (PHAA) PHARMACIA & UPJOHN.
XX
PI Lowery DE, Geary TG, Kubiak TM, Larsen MJ;
XX
DR WPI; 2001-343952/36.
DR N-PSDB; AAS07208.
XX
PT Using G-protein-coupled receptor (GPCR)-like receptors to identify
PT candidate compounds for the treatment and prevention of invertebrate
PT parasites, especially helminths and insects.
XX
PS Claim 6; Page 110-111; 219pp; English.
XX
CC The sequence represents a G protein-coupled receptor-like (GPCR-like)
CC receptor protein. GPCR-like receptors and their associated nucleic acids
CC may be used to identify candidate compounds for their ability to modulate
CC the activity of GPCRs. The sequences therefore are useful for treating
CC and preventing infection by endoparasitic and ectoparasitic invertebrate
CC parasites, especially helminths and insects, and particularly ailments
CC related to aberrant neurological and neuromuscular function
XX
SQ Sequence 450 AA;

Query Match 29.3%; Score 607.5; DB 4; Length 450;
Best Local Similarity 35.3%; Pred. No. 1.4e-54;
Matches 119; Conservative 76; Mismatches 111; Indels 31; Gaps 7;

```
Qy         33 CIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNV 92
              ||:   :  |  :| || | :|  :: ||  : ::|: ||| :: ::   |:| |  |:
Db          9 CIDVNAIL--QQFNDWTVLFEVRLGYSVLYFLILIIGLVGNGLLITSILMRKKL-SVANI 65

Qy         93 FLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLD 152
              ||:||  :||:|  ||:|:||  |  | | || :|| |||   : || ::|||| |::|
Db         66 FLINLAVSDLLLCITAVPITPVLAFMKRWIFGIIMCKLVPTCQAFSVLISSWSLCYIAID 125

Qy        153 KFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDGSFYVQPGET------ 206
              ::  |  | ::| | | |  :    |:|: | : |           :| |  :|
Db        126 RYRSIVTPLREPWSDRHARWLLMFTWVVAFLASYPL----------YYSQNLKTMVIENV 175

Qy        207 PYCGHFCDEANWQSENSRKI-YGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQF 265
              || || | ||||:    |: | |:::::| ::|  ::::||  ||||  | ::
Db        176 TLCGDFCGEFNWQSDEISKLTYTTSLLIIQLIIPAIIMSFCYLMILQKVQTDWLVDEGSM 235

Qy        266 CQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEW-------- 317
              ||  |::    ||::| |:|| ||: |: || ||: :|| :|     |:
Db        236 ---LTAAQQAQTAVRKRRVMYVLILMVIVFMACWFPLSAVNLFRDLGMRFEFCQTVYKVL 292

Qy        318 LKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRS 354
              :  | :|  :| |||||: :||||:|:||:::: :|:
Db        293 MMDQMYFKLLNVHVIAMTSIVWNPVLYFWMSKRHRRA 329
```

RESULT 5
ADN23955
ID ADN23955 standard; protein; 539 AA.
XX
AC ADN23955;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #6608.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.

```
XX
PN   US2003233675-A1.
XX
PD   18-DEC-2003.
XX
PF   20-FEB-2003; 2003US-00369493.
XX
PR   21-FEB-2002; 2002US-0360039P.
XX
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
XX
PI   Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR   WPI; 2004-061375/06.
XX
PT   New recombinant DNA construct comprising a promoter positioned to provide
PT   for expression of a polynucleotide encoding a polypeptide from a
PT   microbial source, useful for producing plants with improved properties.
XX
PS   Claim 1; SEQ ID NO 6608; 122pp; English.
XX
CC   The invention relates to a recombinant DNA construct comprising a
CC   promoter functional in a plant cell, where the promoter is positioned to
CC   provide for expression of a polynucleotide encoding a polypeptide from a
CC   microbial source. The invention also relates to a transformed plant
CC   comprising the recombinant DNA construct and a method of producing a
CC   transformed plant having an improved property. The plant is a crop plant
CC   such as maize or soybean. The method of producing a transformed plant
CC   having an improved property comprises transforming a plant with the
CC   recombinant DNA construct and growing the transformed plant, where the
CC   polynucleotide or polypeptide is useful for improving plant properties.
CC   The recombinant DNA construct is useful for producing plants with
CC   improved plant properties, e.g. improved cold, heat or drought tolerance,
CC   tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC   increased resistance to plant disease, better growth rate by modification
CC   of the cell cycle pathway with plant growth regulators, increased rate of
CC   homologous recombination, modified seed oil or protein yield and/or
CC   content, improved yield by modification of carbohydrate, nitrogen or
CC   phosphorus use and/or uptake, by modification of photosynthesis or by
CC   providing improved plant growth and development under at least one stress
CC   condition, improved lignin production or improved galactomannan
CC   production. This sequence represents a bacterial polypeptide used in the
CC   scope of the invention. Note: The sequence data for this patent did not
CC   form part of the printed specification but was obtained in electronic
CC   format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ   Sequence 539 AA;

  Query Match             29.3%;  Score 607.5;  DB 8;  Length 539;
  Best Local Similarity   35.3%;  Pred. No. 1.8e-54;
  Matches  119;  Conservative   76;  Mismatches  111;  Indels   31;  Gaps    7;

Qy         33 CIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNV 92
              ||  :   :  |  :| || | :|  :: ||  : ::|: ||| :: ::   |:| |  |:
Db          9 CIDVNAIL--QQFNDWTVLFEVRLGYSVLYFLILIIGLVGNGLLITSILMRKKL-SVANI 65

Qy         93 FLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLD 152
              ||:||  :||:|  ||:|:||  |  | | || :|| |||   : || ::|||| |::|
Db         66 FLINLAVSDLLLCITAVPITPVLAFMKRWIFGIIMCKLVPTCQAFSVLISSWSLCYIAID 125

Qy        153 KFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDGSFYVQPGET------ 206
              ::  |  | ::| | | |  :    |:|: | : |           :| |  :|
Db        126 RYRSIVTPLREPWSDRHARWLLMFTWVVAFLASYPL----------YYSQNLKTMVIENV 175

Qy        207 PYCGHFCDEANWQSENSRKI-YGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQF 265
                 || || | ||||:   |: | |:::::| ::|  ::::||  ||||| | ::
Db        176 TLCGDFCGEFNWQSDEISKLTYTTSLLIIQLIIPAIIMSFCYLMILQKVQTDWLVDEGSM 235

Qy        266 CQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEW-------- 317
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                 ||  |::    ||::| |:|| ||: |: || ||: :|| :|     |:
Db        236 ---LTAAQQAQTAVRKRRVMYVLILMVIVFMACWFPLSAVNLFRDLGMRFEFCQTVYKVL 292

Qy        318 LKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRS 354
              :  | :|  :| |||||: :||||:|:||:::: :|:
Db        293 MMDQMYFKLLNVHVIAMTSIVWNPVLYFWMSKRHRRA 329


RESULT 6
AAB86955
ID   AAB86955 standard; protein; 518 AA.
XX
AC   AAB86955;
XX
DT   11-DEC-2001  (first entry)
XX
DE   D. melanogaster peptide receptor SEQ ID 8.
XX
KW   Insect; fruitfly; peptide receptor; plant protection; insecticide.
XX
OS   Drosophila melanogaster.
XX
PN   DE10013618-A1.
XX
PD   20-SEP-2001.
XX
PF   18-MAR-2000; 2000DE-01013618.
XX
PR   18-MAR-2000; 2000DE-01013618.
XX
PA   (FARB ) BAYER AG.
XX
PI   Antonicek H, Friedrich G, Schulte T;
XX
DR   WPI; 2001-571695/65.
DR   N-PSDB; AAH49408.
XX
PT   New polypeptides from Drosophila melanogaster have biological activity of
PT   peptide receptor, useful to find new compounds for plant protection and
PT   insecticides.
XX
PS   Claim 2; Page 28-30; 128pp; German.
XX
CC   This invention describes novel polypeptides (P1) from Drosophila
CC   melanogaster having the biological activity of a peptide receptor.
CC   Molecules of the invention are used to find new plant protection
CC   compounds or insecticides, or to find genes encoding a polypeptide
CC   involved in the structure of functionally similar receptors in insects
CC   This sequence represents a Drosophila melanogaster (fruitfly) peptide
CC   receptor described in the method of the invention
XX
SQ   Sequence 518 AA;

  Query Match             25.5%;  Score 529;  DB 4;  Length 518;
  Best Local Similarity   30.5%;  Pred. No. 3.1e-46;
  Matches  136;  Conservative   76;  Mismatches  154;  Indels   80;  Gaps   12;

Qy          6 ATISTISTTTTPST---------ISNVITSHSNNGSCIQIAEAIAAQGID---DITVDFY 53
              | :| :|| || |:          :|    | :: |:   |   :||   |    |  : :
Db          2 ANLSWLSTITTTSSSISTSQLPLVSTTNWSLTSPGTTSAILADVAASDEDRSGGIIHNQF 61

Qy         54 IRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTP 113
              ::  |  ||  :||||:|||  | : | ||: :|:  |:|: ||  :|::|   |:| ||
Db         62 VQIFFYVLYATVFVLGVFGNVLVCYVVLRNRAMQTVTNIFITNLALSDILLCVLAVPFTP 121

Qy        114 WYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAI 173
               |     ||||  :||||  :  ||:::::: :||:|::|::  |  |    : :   : |
Db        122 LYTFMGRWAFGRSLCHLVSFAQGCSIYISTLTLTSIAIDRYFVIIYPFHPRMKLSTCIGI 181

Qy        174 TFLIWIVSTLINLPYLMSFE---------------------HVDGSFYVQPG-------- 204
                  ||::: |  :|| |  :                    :|||  |
Db        182 IVSIWVIALLATVPYGMYMKMTNELVNGTQTGNETLVEATLMLNGSFVAQGSGFIEAPDS 241
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Qy        205 ------------------ETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYC 246
                                 | ||   :|:| || ||  ||::|     ||||:|  :|: |
Db        242 TSATQAYMQVMTAGSTGPEMPYVRVYCEE-NWPSEQYRKVFGAITTTLQFVLPFFIISIC 300

Qy        247 YFKILQKVSKDMIIQNAQFCQSLTQKQRSDA-TSRKKKVNYILIAMVVTFIGCWLPLTLL 305
              | | |::     | |:       :| :|   |||: | :|||||  |   |||: ::
Db        301 YVWISVKLN-----QRARAKPGSKSSRREEADRDRKKRTNRMLIAMVAVFGLSWLPINVV 355

Qy        306 NLVKDF-KKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLT---RKQKRSGL----- 356
              |:  ||  |  ||     ||:   || ||||   :|| |: ||    ||: :  |
Db        356 NIFDDFDDKSNEWRFYILFFFV--AHSIAMSSTCYNPFLYAWLNENFRKEFKHVLPCFNP 413

Qy        357 --SKILNSTEGSKKAGGSGLRGIQLH 380
                : |:| | |  ::  :   | :||
Db        414 SNNNIINITRGYNRSDRNTC-GPRLH 438
```

RESULT 7
ABB71560
ID ABB71560 standard; protein; 600 AA.
XX
AC ABB71560;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 41472.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR N-PSDB; ABL15663.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 41472; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 600 AA;

Query Match 25.5%; Score 529; DB 4; Length 600;
Best Local Similarity 30.5%; Pred. No. 3.8e-46;
Matches 136; Conservative 76; Mismatches 154; Indels 80; Gaps 12;

```
Qy          6 ATISTISTTTPST---------ISNVITSHSNNGSCIQIAEAIAAQGID---DITVDFY 53
              | :| :|| || |:         :|    | :: |:   |   :||   |    | : :

Db          2 ANLSWLSTITTTSSSISTSQLPLVSTTNWSLTSPGTTSAILADVAASDEDRSGGIIHNQF 61

Qy         54 IRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTP 113
              ::  |  ||  :||||:|||  | : | ||: :|:  |:|: ||  :|::|   |:| ||
Db         62 VQIFFYVLYATVFVLGVFGNVLVCYVVLRNRAMQTVTNIFITNLALSDILLCVLAVPFTP 121

Qy        114 WYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAI 173
                |     |||| :|||| :  ||::::: :||:|::|::  |  |   : :  : |
Db        122 LYTFMGRWAFGRSLCHLVSFAQGCSIYISTLTLTSIAIDRYFVIIYPFHPRMKLSTCIGI 181

Qy        174 TFLIWIVSTLINLPYLMSFE--------------------HVDGSFYVQPG-------- 204
                ||::: |  :|| |  :                     ::|||  |
Db        182 IVSIWVIALLATVPYGMYMKMTNELVNGTQTGNETLVEATLMLNGSFVAQGSGFIEAPDS 241

Qy        205 ------------------ETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYC 246
                               | ||   :|:| || ||  ||::|     ||||:|  :|: |
Db        242 TSATQAYMQVMTAGSTGPEMPYVRVYCEE-NWPSEQYRKVFGAITTTLQFVLPFFIISIC 300

Qy        247 YFKILQKVSKDMIIQNAQFCQSLTQKQRSDA-TSRKKKVNYILIAMVVTFIGCWLPLTLL 305
              | | |::     | |:       :| :|   |||: | :|||||  |   |||: ::
Db        301 YVWISVKLN-----QRARAKPGSKSSRREEADRDRKKRTNRMLIAMVAVFGLSWLPINVV 355

Qy        306 NLVKDF-KKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLT---RKQKRSGL----- 356
              |:  ||  |  ||     ||:   || ||||   :|| |: ||    ||: :  |
Db        356 NIFDDFDDKSNEWRFYILFFFV--AHSIAMSSTCYNPFLYAWLNENFRKEFKHVLPCFNP 413

Qy        357 --SKILNSTEGSKKAGGSGLRGIQLH 380
                : |:| | |  ::  :   | :||
Db        414 SNNNIINITRGYNRSDRNTC-GPRLH 438
```

RESULT 8
AAU03205
ID AAU03205 standard; protein; 600 AA.
XX
AC AAU03205;
XX
DT 12-SEP-2001 (first entry)
XX
DE Fruit fly G protein coupled receptor, DmGPCR1.
XX
KW Fruit fly; G protein coupled receptor; DmGPCR1;
KW human immunodeficiency virus; HIV; cancer; Parkinson's disease; diabetes;
KW obesity; atherosclerosis; thrombosis; stroke; renal failure;
KW inflammation; rheumatoid arthritis; autoimmune disorder;
KW neurological disorder; schizophrenia; manic depression; dementia;
KW severe mental retardation; dyskinesia; Huntington's disease;
KW Tourette's syndrome.
XX
OS Drosophila melanogaster.
XX
PN WO200131005-A2.
XX
PD 03-MAY-2001.
XX
PF 20-OCT-2000; 2000WO-US029002.
XX
PR 22-OCT-1999; 99US-00425676.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Lowery DE, Smith VG, Kubiak TA, Larsen MJ;
XX
DR WPI; 2001-316333/33.
DR N-PSDB; AAS05844.
XX
PT New Drosophila melanogaster GPCR nucleic acids and polypeptide useful for
PT inducing an immune response, for identifying homologs and for treating
PT e.g. diabetes, obesity and manic depression.
XX
PS Claim 29; Page 57; 110pp; English.
XX
CC The sequence represents a fruit fly G protein coupled receptor, DmGPCR1.

CC The proteins are useful for inducing an immune response against itself in
CC a mammal. The nucleic acids are useful for identifying an animal homolog
CC of DmGPCR, by screening databases or libraries. The compounds identified
CC as binding partners or modulators of GPCR binding are useful for treating
CC diseases in animals, and for control insects that are harmful or cause
CC injury to plants or animals. Diseases treated include infections (e.g.
CC viral and human immunodeficiency virus, HIV), cancer, pain, Parkinson's
CC disease, hypotension, hypertension, diabetes, obesity, atherosclerosis,
CC thrombosis, stroke, renal failure, inflammation, rheumatoid arthritis,
CC autoimmune disorders, and psychotic and neurological disorders (anxiety,
CC schizophrenia, manic depression, delirium, dementia, severe mental
CC retardation, dyskinesias, Huntington's disease or Tourette's syndrome).
CC The nucleic acids can be used for genetic mapping, and producing the
CC GPCRs. Anti-GPCR antibodies can be used in therapy, diagnostic assays and
CC for modulating GPCR activity
XX
SQ Sequence 600 AA;

Query Match 25.5%; Score 529; DB 4; Length 600;
Best Local Similarity 30.5%; Pred. No. 3.8e-46;
Matches 136; Conservative 76; Mismatches 154; Indels 80; Gaps 12;

```
Qy          6 ATISTISTTTTPST---------ISNVITSHSNNGSCIQIAEAIAAQGID---DITVDFY 53
              | :| :|| || |:         :|    | :: |:   |   :||   |    |  : :
Db          2 ANLSWLSTITTTSSSISTSQLPLVSTTNWSLTSPGTTSAILADVAASDEDRSGGIIHNQF 61

Qy         54 IRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTP 113
              ::  |  ||  :||||:|||  | : | ||: :|:  |:|: ||  :|::|   |:| ||
Db         62 VQIFFYVLYATVFVLGVFGNVLVCYVVLRNRAMQTVTNIFITNLALSDILLCVLAVPFTP 121

Qy        114 WYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAI 173
              |    ||||  :|||| :  ||::::: :||:|::|::  |  |   : :  : |
Db        122 LYTFMGRWAFGRSLCHLVSFAQGCSIYISTLTLTSIAIDRYFVIIYPFHPRMKLSTCIGI 181

Qy        174 TFLIWIVSTLINLPYLMSFE--------------------HVDGSFYVQPG-------- 204
              ||::: |  :|| |  :                    ::|||  |
Db        182 IVSIWVIALLATVPYGMYMKMTNELVNGTQTGNETLVEATLMLNGSFVAQGSGFIEAPDS 241

Qy        205 ------------------ETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYC 246
                               | ||   :|:| || ||  ||::|     |||:|  :|: |
Db        242 TSATQAYMQVMTAGSTGPEMPYVRVYCEE-NWPSEQYRKVFGAITTTLQFVLPFFIISIC 300

Qy        247 YFKILQKVSKDMIIQNAQFCQSLTQKQRSDA-TSRKKKVNYILIAMVVTFIGCWLPLTLL 305
              |  |  |::     | |:        :| :|   |||: | :|||||  |   |||: ::
Db        301 YVWISVKLN-----QRARAKPGSKSSRREEADRDRKKRTNRMLIAMVAVFGLSWLPINVV 355

Qy        306 NLVKDF-KKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLT---RKQKRSGL----- 356
              |:  ||  |  ||     ||:   || ||||   :|| |: ||    ||: :  |
Db        356 NIFDDFDDKSNEWRFYILFFFV--AHSIAMSSTCYNPFLYAWLNENFRKEFKHVLPCFNP 413

Qy        357 --SKILNSTEGSKKAGGSGLRGIQLH 380
                : |:| | |  ::  :   | :||
Db        414 SNNNIINITRGYNRSDRNTC-GPRLH 438
```

RESULT 9
AAE38182
ID AAE38182 standard; protein; 600 AA.
XX
AC AAE38182;
XX
DT 20-NOV-2003 (first entry)
XX
DE Fruit fly G protein-coupled receptor (GPCR) protein #31.
XX
KW Fruit fly; G protein-coupled receptor; GPCR; cell therapy; nematode;
KW insect infestation; insecticide; nematocide; receptor.
XX
OS Drosophila melanogaster.
XX
PN WO2003052078-A2.
XX
PD 26-JUN-2003.
XX
PF 18-DEC-2002; 2002WO-US040525.
XX
PR 18-DEC-2001; 2001US-0341512P.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Spana E, Kamdar K, Stam L, Valentine S, Griswold CM;
XX
DR WPI; 2003-533019/50.
DR N-PSDB; AAD57459.
XX
PT New polypeptide, useful for preventing or abrogating insect or nematode
PT infestation of a plant.
XX
PS Claim 1; Page 239-242; 368pp; English.
XX
CC The invention relates to a novel G protein-coupled receptor (GPCR)
CC polypeptide and its polynucleotide. The polypeptide is useful for
CC preventing or abrogating insect or nematode infestation of a plant. GPCR
CC polypeptide is useful in cell therapy. The present sequence is fruit fly
CC GPCR protein
XX
SQ Sequence 600 AA;

Query Match 25.5%; Score 529; DB 7; Length 600;
Best Local Similarity 30.5%; Pred. No. 3.8e-46;
Matches 136; Conservative 76; Mismatches 154; Indels 80; Gaps 12;

```
Qy          6 ATISTISTTTTPST---------ISNVITSHSNNGSCIQIAEAIAAQGID---DITVDFY 53
              | :| :|| || |:         :|    | :: |:   |   :||   |    |  : :
Db          2 ANLSWLSTITTTSSSISTSQLPLVSTTNWSLTSPGTTSAILADVAASDEDRSGGIIHNQF 61

Qy         54 IRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTP 113
              ::  |  ||  :||||:|||  | : | ||: :|:  |:|: ||  :|::|   |:| ||
Db         62 VQIFFYVLYATVFVLGVFGNVLVCYVVLRNRAMQTVTNIFITNLALSDILLCVLAVPFTP 121

Qy        114 WYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAI 173
              |    ||||  :|||| :  ||::::: :||:|::|::  |  |   : :  : |
Db        122 LYTFMGRWAFGRSLCHLVSFAQGCSIYISTLTLTSIAIDRYFVIIYPFHPRMKLSTCIGI 181

Qy        174 TFLIWIVSTLINLPYLMSFE--------------------HVDGSFYVQPG-------- 204
              ||::: |  :|| |  :                      ::|||  |
Db        182 IVSIWVIALLATVPYGMYMKMTNELVNGTQTGNETLVEATLMLNGSFVAQGSGFIEAPDS 241

Qy        205 ------------------ETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYC 246
                               | ||   :|:| || ||  ||::|     |||:|  :|: |
Db        242 TSATQAYMQVMTAGSTGPEMPYVRVYCEE-NWPSEQYRKVFGAITTTLQFVLPFFIISIC 300

Qy        247 YFKILQKVSKDMIIQNAQFCQSLTQKQRSDA-TSRKKKVNYILIAMVVTFIGCWLPLTLL 305
              |  |  |::     | |:        :| :|   |||: | :|||||  |   |||: ::
Db        301 YVWISVKLN-----QRARAKPGSKSSRREEADRDRKKRTNRMLIAMVAVFGLSWLPINVV 355

Qy        306 NLVKDF-KKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLT---RKQKRSGL----- 356
              |:  ||  |  ||     ||:   || ||||   :|| |: ||    ||: :  |
Db        356 NIFDDFDDKSNEWRFYILFFFV--AHSIAMSSTCYNPFLYAWLNENFRKEFKHVLPCFNP 413

Qy        357 --SKILNSTEGSKKAGGSGLRGIQLH 380
                : |:| | |  ::  :   | :||
Db        414 SNNNIINITRGYNRSDRNTC-GPRLH 438
```

RESULT 10
ADL83372
ID ADL83372 standard; protein; 600 AA.
XX
AC ADL83372;
XX
DT 20-MAY-2004 (first entry)
XX
DE Drosophila G protein coupled receptor 1 (DmGPCR1).
XX
KW pesticide; neuroprotective; nootropic; antiparkinsonian;

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KW   G protein coupled receptor; DmGPCR1; DmGPCR1 binding partner;
KW   insect population control; ectoparasite; Alzheimer's disease;
KW   Parkinson's disease; Huntington's disease; neuromuscular disease;
KW   neurodegenerative disease; fruit fly; receptor.
XX
OS   Drosophila melanogaster.
XX
PN   US2003162223-A1.
XX
PD   28-AUG-2003.
XX
PF   30-OCT-2002; 2002US-00283423.
XX
PR   22-OCT-1999;   99US-00425676.
PR   20-OCT-2000; 2000US-00693746.
PR   06-AUG-2002; 2002US-00213821.
XX
PA   (LOWE/) LOWERY D E.
PA   (SMIT/) SMITH V G.
PA   (KUBI/) KUBIAK T M.
PA   (LARS/) LARSEN M J.
XX
PI   Lowery DE,  Smith VG,  Kubiak TM,  Larsen MJ;
XX
DR   WPI; 2003-897924/82.
DR   N-PSDB; ADL83601.
XX
PT   Identifying a modulator of binding and/or function between a Drosophila
PT   melanogaster G protein coupled receptor and it's binding partner is
PT   useful to control insect populations and prevent or treat disease due to
PT   ectoparasites.
XX
PS   Disclosure; SEQ ID NO 2; 52pp; English.
XX
CC   The invention describes a method of identifying a modulator of binding
CC   and/or function between a Drosophila melanogaster G protein coupled
CC   receptor (DmGPCR1) and a DmGPCR1 binding partner, comprising contacting
CC   DmGPCR and the binding partner in the presence of a candidate compound
CC   and determining the effect of the compound on binding and/or function.
CC   Also described are: a method for controlling a population of insects; and
CC   a method of treating or preventing a disease or condition caused by an
CC   ectoparasite. The invention is used to control insects, particularly
CC   flies, tick, fleas, lice, mites or cockroaches and to prevent or treat a
CC   disease caused by an ectoparasite, particularly Alzheimer's, Parkinson's,
CC   Huntington's disease and other neuromuscular and neurodegenerative
CC   diseases. This is the amino acid sequence of Drosophila melanogaster G
CC   protein coupled receptor 1 (DmGPCR1).
XX
SQ   Sequence 600 AA;

  Query Match             25.5%;  Score 529;  DB 7;  Length 600;
  Best Local Similarity   30.5%;  Pred. No. 3.8e-46;
  Matches  136;  Conservative   76;  Mismatches  154;  Indels   80;  Gaps   12;

Qy          6 ATISTISTTTTPST---------ISNVITSHSNNGSCIQIAEAIAAQGID---DITVDFY 53
              | :| :|| || |:         :|    | :: |:   |   :||   |    |  : :
Db          2 ANLSWLSTITTTSSSISTSQLPLVSTTNWSLTSPGTTSAILADVAASDEDRSGGIIHNQF 61

Qy         54 IRSIFTFLYGPLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTP 113
              ::  |  ||  :||||:|||  | : | ||: :|:  |:|: ||  :|::|   |:| ||
Db         62 VQIFFYVLYATVFVLGVFGNVLVCYVVLRNRAMQTVTNIFITNLALSDILLCVLAVPFTP 121

Qy        114 WYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAI 173
               |    ||||  :|||| :  ||::::: :||:|::|::  |  |    : :   : |
Db        122 LYTFMGRWAFGRSLCHLVSFAQGCSIYISTLTLTSIAIDRYFVIIYPFHPRMKLSTCIGI 181

Qy        174 TFLIWIVSTLINLPYLMSFE--------------------HVDGSFYVQPG-------- 204
                ||::: |  :|| |  :                    ::|||  |
Db        182 IVSIWVIALLATVPYGMYMKMTNELVNGTQTGNETLVEATLMLNGSFVAQGSGFIEAPDS 241

Qy        205 -----------------ETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYC 246
                             | ||   :|:| || ||  ||::|     ||||:|  :|: |
Db        242 TSATQAYMQVMTAGSTGPEMPYVRVYCEE-NWPSEQYRKVFGAITTTLQFVLPFFIISIC 300

Qy        247 YFKILQKVSKDMIIQNAQFCQSLTQKQRSDA-TSRKKKVNYILIAMVVTFIGCWLPLTLL 305
              | |  |::     | |:         :| :|   |||: | :|||||  |   |||: ::
Db        301 YVWISVKLN-----QRARAKPGSKSSRREEADRDRKKRTNRMLIAMVAVFGLSWLPINVV 355

Qy        306 NLVKDF-KKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLT---RKQKRSGL----- 356
              |:  ||  |  ||      ||:   || ||||   :|| |: ||    ||: :  |
Db        356 NIFDDFDDKSNEWRFYILFFFV--AHSIAMSSTCYNPFLYAWLNENFRKEFKHVLPCFNP 413

Qy        357 --SKILNSTEGSKKAGGSGLRGIQLH 380
                : |:| | |  ::  :   | :||
Db        414 SNNNIINITRGYNRSDRNTC-GPRLH 438


RESULT 11
ADR03092
ID   ADR03092 standard; protein; 600 AA.
XX
AC   ADR03092;
XX
DT   23-SEP-2004  (first entry)
XX
DE   Drosophila G-protein coupled receptor DmGPCR1.
XX
KW   antiasthmatic; antiarteriosclerotic; neuroprotective; antiinflammatory;
KW   gastrointestinal; atipsoriatic; antiarthritic; antirheumatic;
KW   antithyroid; immunosuppressive; cardiant; cerebroprotective; vasotropic;
KW   nephrotropic; cytostatic; insecticide; immune response;
KW   G-protein coupled receptor; cancer; tumour growth; asthma; psoriasis;
KW   inflammatory bowel disease; multiple sclerosis; thyroiditis;
KW   rheumatoid arthritis; metabolic disorder; artherosclerosis;
KW   autoimmune disorder; organ transplantation; myocardial infarction;
KW   cardiomyopathy; stroke; renal failure;
KW   oxidative stress-related neurodegenerative disorder; fruit fly; DmGPCR1;
KW   receptor.
XX
OS   Drosophila melanogaster.
XX
PN   US2004121956-A1.
XX
PD   24-JUN-2004.
XX
PF   15-DEC-2003; 2003US-00736048.
XX
PR   22-OCT-1999;   99US-00425676.
PR   20-OCT-2000; 2000US-00693746.
XX
PA   (LOWE/) LOWERY D E.
PA   (SMIT/) SMITH V G.
PA   (KUBI/) KUBIAK T M.
PA   (LARS/) LARSEN M J.
XX
PI   Lowery DE,  Smith VG,  Kubiak TM,  Larsen MJ;
XX
DR   WPI; 2004-468193/44.
DR   N-PSDB; ADR03091.
XX
PT   Novel isolated nucleic acid molecule encoding Drosophila melanogaster G-
PT   protein coupled receptor (DmGPCR), useful in screening DmGPCR modulators
PT   for treating disorders e.g. artherosclerosis, myocardial infarction,
PT   stroke and cardiomyopathy.
XX
PS   Claim 29; SEQ ID NO 2; 101pp; English.
XX
CC   The invention describes a nucleic acid molecule encoding Drosophila
CC   melanogaster G-protein coupled receptor, having fully defined sequence
CC   (S1) of 1803, 1443, 1376, 1559, 1568, 1394, 1556,1628, 1451, 1754 or 1452
CC   nucleotides as given in specification, a sequence that encodes protein
CC   having fully defined sequence (S2) of 600, 357, 458, 519, 522, 518, 542,
CC   483, 584 or 483 amino acids as given in specification, or a sequence
CC   complementary to (S1). Also described are: an expression vector (II)
CC   comprising (I); a host cell (III) transformed with (II); an isolated
CC   polypeptide (IV) encoded by (I); an isolated antibody (V) binding to an
```

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CC   epitope on (IV); a compound (VI) modulating to (I) or (IV); and a
CC   composition (VII) comprising (I), (II), (IV) or (V) and a carrier or
CC   diluent. (I) is useful for identifying a compound which binds (I) and
CC   identifying an animal homologue of (I). (II) is useful in producing (IV)
CC   or a homologue or their fragment. (IV) is useful for inducing an immune
CC   response in a mammal against (IV) and in identifying a compound binding
CC   to (IV). (IV) is useful in identifying a compound that modulates the
CC   activity of (IV) and in identifying a modulator of binding between (IV)
CC   and a DmGPCR binding partner. (I), (IV), (V) or (VI) is useful in
CC   treating cancer cell, tumour growth. (I) or (IV) is useful in treating
CC   asthma, psoriasis, inflammatory bowel disease, multiple sclerosis,
CC   thyroiditis, rheumatoid arthritis. (VI) is useful in treating a disease
CC   or abnormal condition such as metabolic disorder, rheumatoid arthritis,
CC   artherosclerosis, autoimmune disorder, organ transplantation, myocardial
CC   infarction, cardiomyopathy, stroke, renal failure, oxidative stress-
CC   related neurodegenerative disorders and cancer. (VI) is useful for
CC   treating disease in animals and for control of insect that are injurious
CC   or harmful to plants or animals. This is the amino acid sequence of
CC   Drosophila G-protein coupled receptor DmGPCR1.
XX
SQ   Sequence 600 AA;

  Query Match             25.5%;  Score 529;  DB 8;  Length 600;
  Best Local Similarity   30.5%;  Pred. No. 3.8e-46;
  Matches  136;  Conservative   76;  Mismatches  154;  Indels   80;  Gaps   12;

Qy          6 ATISTISTTTTPST---------ISNVITSHSNNGSCIQIAEAIAAQGID---DITVDFY 53
              | :| :|| || |:         :|    | :: |:   |   :||   |    |  : :
Db          2 ANLSWLSTITTTSSSISTSQLPLVSTTNWSLTSPGTTSAILADVAASDEDRSGGIIHNQF 61

Qy         54 IRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTP 113
              ::  |  ||  :||||:|||  | : | ||: :|:  |:|: ||  :|::|   |:| ||
Db         62 VQIFFYVLYATVFVLGVFGNVLVCYVVLRNRAMQTVTNIFITNLALSDILLCVLAVPFTP 121

Qy        114 WYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAI 173
               |    ||||  :|||  :  ||:::: :||:|::|::  |  |    : :   : |
Db        122 LYTFMGRWAFGRSLCHLVSFAQGCSIYISTLTLTSIAIDRYFVIIYPFHPRMKLSTCIGI 181

Qy        174 TFLIWIVSTLINLPYLMSFE--------------------HVDGSFYVQPG-------- 204
              ||::: |  :|| |  :                      ::|||  |
Db        182 IVSIWVIALLATVPYGMYMKMTNELVNGTQTGNETLVEATLMLNGSFVAQGSGFIEAPDS 241

Qy        205 ------------------ETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYC 246
                               | ||   :|:| || ||  ||::|     ||||:|  :|: |
Db        242 TSATQAYMQVMTAGSTGPEMPYVRVYCEE-NWPSEQYRKVFGAITTTLQFVLPFFIISIC 300

Qy        247 YFKILQKVSKDMIIQNAQFCQSLTQKQRSDA-TSRKKKVNYILIAMVVTFIGCWLPLTLL 305
              |  |  |::     | |:         :| :|   |||: | :|||||  |   |||: ::
Db        301 YVWISVKLN-----QRARAKPGSKSSRREEADRDRKKRTNRMLIAMVAVFGLSWLPINVV 355

Qy        306 NLVKDF-KKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLT---RKQKRSGL----- 356
              |:  ||  |  ||     ||:   || ||||   :|| |: ||    ||: :  |
Db        356 NIFDDFDDKSNEWRFYILFFFV--AHSIAMSSTCYNPFLYAWLNENFRKEFKHVLPCFNP 413

Qy        357 --SKILNSTEGSKKAGGSGLRGIQLH 380
                : |:| | |  ::  :   | :||
Db        414 SNNNIINITRGYNRSDRNTC-GPRLH 438


RESULT 12
ADV91972
ID   ADV91972 standard; protein; 600 AA.
XX
AC   ADV91972;
XX
DT   10-MAR-2005  (first entry)
XX
DE   DmGPCR1, SEQ ID 2.
XX
KW   Virucide; Antiinflammatory; Anti-HIV; Antiparkinsonian; Hypotensive;
KW   Hypertensive; Antidiabetic; Antirheumatic; Antiarthritic; Anorectic;
KW   Antiarteriosclerotic; Thrombolytic; Cerebroprotective; Vasotropic;
KW   Immunosuppressive; Analgesic; Cytostatic; Nephrotropic; Neuroleptic;
KW   Neuroprotective; viral infection; HIV infection; pain; cancer;
KW   Parkinsons disease; hypotension; hypertension; diabetes; obesity;
KW   atherosclerosis; thrombosis; cerebrovascular ischemia; renal failure;
KW   inflammation; rheumatoid arthritis; autoimmune disease;
KW   psychotic disorder; neurological disease; G-protein coupled receptor;
KW   DmGPCR.
XX
OS   Drosophila melanogaster.
XX
PN   US6835546-B1.
XX
PD   28-DEC-2004.
XX
PF   20-OCT-2000; 2000US-00693746.
XX
PR   22-OCT-1999;   99US-00425676.
XX
PA   (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI   Lowery DE,  Smith VG,  Kubiak TM,  Larsen MJ;
XX
DR   WPI; 2005-077883/09.
DR   N-PSDB; ADV91971.
XX
PT   Identifying modulator of Drosophila melanogaster G-protein coupled
PT   receptor (DmGPCR) useful for treating diseases such as cancer, obesity,
PT   etc., by determining effect of modulator on binding between DmGPCR and
PT   DmGPCR binding partner.
XX
PS   Disclosure; SEQ ID NO 2; 92pp; English.
XX
CC   The present invention relates to a method (M1) for identifying a
CC   modulator of binding between a Drosophila melanogaster G-protein coupled
CC   receptor (DmGPCR) and a DmGPCR binding partner. The method involves
CC   contacting a DmGPCR binding partner and a composition comprising a DmGPCR
CC   in the presence and absence of a putative modulator compound; detecting
CC   binding between the binding partner and the DmGPCR and determining
CC   whether binding in the presence of the putative modulator is increased or
CC   decreased compared to binding in absence of modulator. DmGPCR modulators
CC   identified by (M1) are useful for treating diseases such as viral
CC   infection caused by HIV-1 or HIV-2, pain, cancer, Parkinson's disease,
CC   hypotension, hypertension, diabetes, obesity, atherosclerosis,
CC   thrombosis, stroke, renal failure, inflammation, rheumatoid arthritis,
CC   autoimmune disorder or psychotic and neurological disorder. The present
CC   sequence is one such DmGPCR.
XX
SQ   Sequence 600 AA;

  Query Match             25.5%;  Score 529;  DB 9;  Length 600;
  Best Local Similarity   30.5%;  Pred. No. 3.8e-46;
  Matches  136;  Conservative   76;  Mismatches  154;  Indels   80;  Gaps   12;

Qy          6 ATISTISTTTTPST---------ISNVITSHSNNGSCIQIAEAIAAQGID---DITVDFY 53
              | :| :|| || |:         :|    | :: |:   |   :||   |    |  : :
Db          2 ANLSWLSTITTTSSSISTSQLPLVSTTNWSLTSPGTTSAILADVAASDEDRSGGIIHNQF 61

Qy         54 IRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTP 113
              ::  |  ||  :||||:|||  | : | ||: :|:  |:|: ||  :|::|   |:| ||
Db         62 VQIFFYVLYATVFVLGVFGNVLVCYVVLRNRAMQTVTNIFITNLALSDILLCVLAVPFTP 121

Qy        114 WYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAI 173
               |    ||||  :|||  :  ||:::: :||:|::|::  |  |    : :   : |
Db        122 LYTFMGRWAFGRSLCHLVSFAQGCSIYISTLTLTSIAIDRYFVIIYPFHPRMKLSTCIGI 181

Qy        174 TFLIWIVSTLINLPYLMSFE--------------------HVDGSFYVQPG-------- 204
              ||::: |  :|| |  :                      ::|||  |
Db        182 IVSIWVIALLATVPYGMYMKMTNELVNGTQTGNETLVEATLMLNGSFVAQGSGFIEAPDS 241

Qy        205 ------------------ETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYC 246
                               | ||   :|:| || ||  ||::|     ||||:|  :|: |
Db        242 TSATQAYMQVMTAGSTGPEMPYVRVYCEE-NWPSEQYRKVFGAITTTLQFVLPFFIISIC 300

Qy        247 YFKILQKVSKDMIIQNAQFCQSLTQKQRSDA-TSRKKKVNYILIAMVVTFIGCWLPLTLL 305
```

```
Db        301 YVWISVKLN-----QRARAKPGSKSSRREEADRDRKKRTNRMLIAMVAVFGLSWLPINVV 355

Qy        306 NLVKDF-KKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLT---RKQKRSGL----- 356
Db        356 NIFDDFDDKSNEWRFYILFFFV--AHSIAMSSTCYNPFLYAWLNENFRKEFKHVLPCFNP 413

Qy        357 --SKILNSTEGSKKAGGSGLRGIQLH 380
Db        414 SNNNIIINITRGYNRSDRNTC-GPRLH 438


RESULT 13
ADE14524
ID   ADE14524 standard; protein; 600 AA.
XX
AC   ADE14524;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Fruit fly G-protein coupled receptor, DmGPCR1.
XX
KW   fruit fly; G-protein coupled receptor; DmGPCR; insect populatio control;
KW   fly; tick; mite; flea; cockroach; ectoparasite; receptor.
XX
OS   Drosophila melanogaster.
XX
PN   US2003180297-A1.
XX
PD   25-SEP-2003.
XX
PF   06-AUG-2002; 2002US-00213821.
XX
PR   22-OCT-1999;   99US-00425676.
PR   20-OCT-2000; 2000US-00693746.
XX
PA   (LOWE/) LOWERY D E.
PA   (SMIT/) SMITH V G.
PA   (KUBI/) KUBIAK T M.
PA   (LARS/) LARSEN M J.
XX
PI   Lowery DE,  Smith VG,  Kubiak TM,  Larsen MJ;
XX
DR   WPI; 2003-843918/78.
DR   N-PSDB; ADE14523.
XX
PT   Binding a Drosophila melanogaster G-protein coupled receptor with a
PT   binding partner or modulator is useful to control an insect population or
PT   to treat or prevent a disease or condition caused by ectoparasites.
XX
PS   Disclosure; SEQ ID NO 2; 53pp; English.
XX
CC   The invention relates to a method of binding a Drosophila melanogaster G-
CC   protein coupled receptor (DmGPCR) with a DmGPCR binding partner. The
CC   invention is used to control an insect population, particularly a fly,
CC   fruit fly, tick, mite, flea or cockroach population, or to treat or
CC   prevent a disease or condition caused by ectoparasites, particularly in a
CC   companion animal, livestock, horse or a human. The present sequence
CC   represents the amino acid sequence of a Drosophila melanogaster G-protein
CC   coupled receptor, DmGPCR.
XX
SQ   Sequence 600 AA;

  Query Match             25.1%;  Score 521;  DB 7;  Length 600;
  Best Local Similarity   30.4%;  Pred. No. 2.7e-45;
  Matches  136;  Conservative   76;  Mismatches  152;  Indels   84;  Gaps   13;

Qy          6 ATISTISTTTTPST---------ISNVITSHSNNGSCIQIAEAIAAQGIDD-----ITVD 51
Db          2 ANLSWLSTITTTSSSISTSQLPLVSTTNWSLTSPGTTSAILADVAAS--DEXRSGGIIHN 59

Qy         52 FYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPV 111
Db         60 QFVQIFFYVLYATVFVLGVFGNVLVCYVVLRNRAMQTVTNIFITNLALSDILLCVLAVPF 119

Qy        112 TPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQAL 171
Db        120 TPLYTFMGRWAFGRSLCHLVSFAQGCSIYISTLTLTSIATDRYFVIIYPFHPRMKLSTCI 179

Qy        172 AITFLIWIVSTLINLPYLMSFE--------------------HVDGSFYVQPG------ 204
Db        180 GIIVSIWVIALLATVPYGMYMKMTNELVNGTQTGNETLVEATLMLNGSFVAQGSGFIEAP 239

Qy        205 --------------------ETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVIT 244
Db        240 DSTSATQAYMQVMTAGSTGPEMPYVRVYCEE-NWPSEQYRKVFGAITTTLQFVLPFFIIS 298

Qy        245 YCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDA-TSRKKKVNYILIAMVVTFIGCWLPLT 303
Db        299 ICYVWISVKLN-----QRARAKPGSKSSRREEADRDRKKRTNRMLIAMVAVFGLSWLPIN 353

Qy        304 LLNLVKDF-KKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLT---RKQKRSGL--- 356
Db        354 VVNIFDDFDDKSNEWRFYILFFFV--AHSIAMSSTCYNPFLYAWLNENFRKEFKHVLPCF 411

Qy        357 ----SKILNSTEGSKKAGGSGLRGIQLH 380
Db        412 NPSNNNIIINITRGYNRSDRNTC-GPRLH 438


RESULT 14
AAU03811
ID   AAU03811 standard; protein; 376 AA.
XX
AC   AAU03811;
XX
DT   12-SEP-2001  (first entry)
XX
DE   G protein-coupled receptor-like (GPCR-like) receptor protein #10.
XX
KW   G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;
KW   endoparasite; ectoparasite; invertebrate; insect; neurological disorder;
KW   neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech;
KW   fruitfly.
XX
OS   Homo sapiens.
XX
PN   WO200138533-A2.
XX
PD   31-MAY-2001.
XX
PF   24-NOV-2000; 2000WO-US032225.
XX
PR   24-NOV-1999;   99US-0167523P.
XX
PA   (PHAA ) PHARMACIA & UPJOHN.
XX
PI   Lowery DE,  Geary TG,  Kubiak TM,  Larsen MJ;
XX
DR   WPI; 2001-343952/36.
DR   N-PSDB; AAS07210.
XX
PT   Using G-protein-coupled receptor (GPCR)-like receptors to identify
PT   candidate compounds for the treatment and prevention of invertebrate
PT   parasites, especially helminths and insects.
XX
PS   Claim 6; Page 118-119; 219pp; English.
XX
CC   The sequence represents a G protein-coupled receptor-like (GPCR-like)
CC   receptor protein. GPCR-like receptors and their associated nucleic acids
CC   may be used to identify candidate compounds for their ability to modulate
CC   the activity of GPCRs. The sequences therefore are useful for treating
CC   and preventing infection by endoparasitic and ectoparasitic invertebrate
CC   parasites, especially helminths and insects, and particularly ailments
CC   related to aberrant neurological and neuromuscular function
XX
```

```
SQ   Sequence 376 AA;

  Query Match             24.9%;  Score 515.5;  DB 4;  Length 376;
  Best Local Similarity   30.3%;  Pred. No. 5.3e-45;
  Matches  119;  Conservative   78;  Mismatches  131;  Indels   65;  Gaps   11;

Qy         29 NNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQS 88
              |   |: :   :     :|::  :||  :| |||  :   || ||  |: |: ||| ||:
Db          2 NGSDCLNLNSELWLYR-EDLSSRWYIMLVFAFLYLIIIAAGIIGNSCVILAITRNKSLQT 60

Qy         89 ARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTA 148
               |:|:|:|  :|:::  |:  :||  |  |:| ||  :| : |      |:  ::::|||
Db         61 VPNLFILSLSCSDIVVCCTSATITPITAFKKEWIFGEALCRIAPFIAGISLCFSTFTLTA 120

Qy        149 ISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDGSFYVQPGETPY 208
              ||:|::: |  | ::|::  ||: :  :|   :  |  | :  |:   | |        :
Db        121 ISIDRYILIRFPMRKPITHYQAVGVIAIICAFAATITSPIM--FKQKLGEF------ENF 172

Qy        209 CGHFCDEANW-QSENSRKIYGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQFCQ 267
              || :| | ||  :|: |||||  :| || |:|: :|   |  |  |: : ||:: |
Db        173 CGQYCTE-NWGANESQRKIYGAALMFLQLVIPLTIIIISYTAISLKIGQSMILKGA---- 227

Qy        268 SLTQKQRSD-----------ATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEP 315
                 :||::|            |  |::: | :|| ||| |   |:     |:::|::  |
Db        228 ---KKQKTDNWEMELSDQQRIAVKRRQRTNRMLIGMVVAFACSWIWSVTFNILRDYEYLP 284

Qy        316 EWLKRQPFFWAINAHVIAMSLVVWNPLLF----------------FWLTRKQKRSG--LS 357
              | :| | : : |  | |||:  ||||||:                || |      |  |
Db        285 ELIKTQEYIFGIATHCIAMTSTVWNPLLYAVLNLQLRAAFIDLMPHWLRRHLNLEGDNSS 344

Qy        358 KILN------STEGSKKAGGSGLRGIQLHDLLP 384
               :||      : : ||:           | |:|
Db        345 PLLNHPTMTITNKPSKQ----------HTLIP 366


RESULT 15
ADN24291
ID   ADN24291 standard; protein; 374 AA.
XX
AC   ADN24291;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Bacterial polypeptide #6944.
XX
KW   Recombinant DNA construct; transformed plant; improved plant property;
KW   cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW   pathogen tolerance; pest tolerance; plant disease resistance;
KW   cell cycle pathway modification; plant growth regulator;
KW   homologous recombination; seed oil yield; protein yield; carbohydrate;
KW   nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW   bacterial polypeptide.
XX
OS   Bacteria.
XX
PN   US2003233675-A1.
XX
PD   18-DEC-2003.
XX
PF   20-FEB-2003; 2003US-00369493.
XX
PR   21-FEB-2002; 2002US-0360039P.
XX
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
XX
PI   Cao Y,  Hinkle GJ,  Slater SC,  Chen X,  Goldman BS;
XX
DR   WPI; 2004-061375/06.
XX
PT   New recombinant DNA construct comprising a promoter positioned to provide
PT   for expression of a polynucleotide encoding a polypeptide from a
PT   microbial source, useful for producing plants with improved properties.
XX
PS   Claim 1; SEQ ID NO 6944; 122pp; English.
XX
CC   The invention relates to a recombinant DNA construct comprising a
CC   promoter functional in a plant cell, where the promoter is positioned to
CC   provide for expression of a polynucleotide encoding a polypeptide from a
CC   microbial source. The invention also relates to a transformed plant
CC   comprising the recombinant DNA construct and a method of producing a
CC   transformed plant having an improved property. The plant is a crop plant
CC   such as maize or soybean. The method of producing a transformed plant
CC   having an improved property comprises transforming a plant with the
CC   recombinant DNA construct and growing the transformed plant, where the
CC   polynucleotide or polypeptide is useful for improving plant properties.
CC   The recombinant DNA construct is useful for producing plants with
CC   improved plant properties, e.g. improved cold, heat or drought tolerance,
CC   tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC   increased resistance to plant disease, better growth rate by modification
CC   of the cell cycle pathway with plant growth regulators, increased rate of
CC   homologous recombination, modified seed oil or protein yield and/or
CC   content, improved yield by modification of carbohydrate, nitrogen or
CC   phosphorus use and/or uptake, by modification of photosynthesis or by
CC   providing improved plant growth and development under at least one stress
CC   condition, improved lignin production or improved galactomannan
CC   production. This sequence represents a bacterial polypeptide used in the
CC   scope of the invention. Note: The sequence data for this patent did not
CC   form part of the printed specification but was obtained in electronic
CC   format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ   Sequence 374 AA;

  Query Match             24.8%;  Score 514;  DB 8;  Length 374;
  Best Local Similarity   31.3%;  Pred. No. 7.6e-45;
  Matches  114;  Conservative   74;  Mismatches  128;  Indels   48;  Gaps    9;

Qy         29 NNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQS 88
              |   |: :   :     :|::  :||  :| |||  :   || ||  |: |: ||| ||:
Db          2 NGSDCLNLNSELWLYR-EDLSSRWYIMLVFAFLYLIIIAAGIIGNSCVILAITRNKSLQT 60

Qy         89 ARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTA 148
               |:|:|:|  :|:::  |:  :||  |  |:| ||  :| : |      |:  ::::|||
Db         61 VPNLFILSLSCSDIVVCCTSATITPITAFKKEWIFGEALCRIAPFIAGISLCFSTFTLTA 120

Qy        149 ISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDGSFYVQPGETPY 208
              ||:|::: |  | ::|::  ||: :  :|   :  |  | :  |:   | |        :
Db        121 ISIDRYILIRFPMRKPITHYQAVGVIAIICAFAATITSPIM--FKQKLGEF------ENF 172

Qy        209 CGHFCDEANW-QSENSRKIYGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQFCQ 267
              || :| | ||  :|: |||||  :| || |:|: :|   |  |  |: : ||:: |
Db        173 CGQYCTE-NWGANESQRKIYGAALMFLQLVIPLTIIIISYTAISLKIGQSMILKGA---- 227

Qy        268 SLTQKQRSD-----------ATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEP 315
                 :||::|            |  |::: | :|| ||| |   |:     |:::|::  |
Db        228 ---KKQKTDNWEMELSDQQRIAVKRRQRTNRMLIGMVVAFACSWIWSVTFNILRDYEYLP 284

Qy        316 EWLKRQPFFWAINAHVIAMSLVVWNPLLF----------------FWLTRKQKRSG--LS 357
              | :| | : : |  | |||:  ||||||:                || |      |  |
Db        285 ELIKTQEYIFGIATHCIAMTSTVWNPLLYAVLNLQLRAAFIDLMPHWLRRHLNLEGDNSS 344

Qy        358 KILN 361
               :||
Db        345 PLLN 348


Search completed: May  8, 2006, 09:29:35
Job time : 191 secs
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OM protein - protein search, using sw model

Run on: May 8, 2006, 09:34:27 ; Search time 166 Seconds
(without alignments)
999.267 Million cell updates/sec

Title: US-10-650-467-105
Perfect score: 2074
Sequence: 1 MVSSAATISTISTTTTPSTI.....QLHDLLPTSTHSDRCAGNSF 397

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2074	100.0	397	5	US-10-650-467-105	Sequence 105, App
2	2074	100.0	499	5	US-10-650-467-40	Sequence 40, Appl
3	1899	91.6	433	5	US-10-650-467-107	Sequence 107, App
4	607.5	29.3	450	5	US-10-650-467-16	Sequence 16, Appl
5	607.5	29.3	539	4	US-10-369-493-6608	Sequence 6608, Ap
6	529	25.5	518	3	US-09-804-551B-8	Sequence 8, Appli
7	529	25.5	600	4	US-10-283-423-2	Sequence 2, Appli
8	529	25.5	600	4	US-10-213-821-2	Sequence 2, Appli
9	529	25.5	600	4	US-10-736-048-2	Sequence 2, Appli
10	529	25.5	600	5	US-10-489-425-62	Sequence 62, Appl
11	529	25.5	600	6	US-11-097-143-41472	Sequence 41472, A
12	515.5	24.9	376	5	US-10-650-467-22	Sequence 22, Appl
13	514	24.8	374	4	US-10-369-493-6944	Sequence 6944, Ap
14	485.5	23.4	457	4	US-10-369-493-6769	Sequence 6769, Ap
15	485.5	23.4	457	5	US-10-650-467-26	Sequence 26, Appl
16	461.5	22.3	365	4	US-10-369-493-6958	Sequence 6958, Ap
17	461.5	22.3	365	5	US-10-650-467-36	Sequence 36, Appl
18	460.5	22.2	387	5	US-10-650-467-14	Sequence 14, Appl
19	458	22.1	381	5	US-10-650-467-12	Sequence 12, Appl
20	458	22.1	402	5	US-10-650-467-8	Sequence 8, Appli
21	458	22.1	404	5	US-10-650-467-6	Sequence 6, Appli
22	458	22.1	406	5	US-10-650-467-10	Sequence 10, Appl
23	419.5	20.2	412	4	US-10-369-493-6883	Sequence 6883, Ap
24	390.5	18.8	375	4	US-10-081-810-51	Sequence 51, Appl
25	388	18.7	458	4	US-10-283-423-6	Sequence 6, Appli
26	388	18.7	458	4	US-10-213-821-6	Sequence 6, Appli
27	388	18.7	458	4	US-10-736-048-6	Sequence 6, Appli
28	387.5	18.7	373	4	US-10-369-493-6097	Sequence 6097, Ap
29	386.5	18.6	380	4	US-10-611-210-11	Sequence 11, Appl
30	386	18.6	370	3	US-09-799-955-5	Sequence 5, Appli
31	386	18.6	370	4	US-10-044-592-12	Sequence 12, Appl
32	386	18.6	370	4	US-10-044-592-74	Sequence 74, Appl
33	386	18.6	370	4	US-10-225-567A-245	Sequence 245, App
34	386	18.6	370	4	US-10-278-087A-26	Sequence 26, Appl
35	386	18.6	370	4	US-10-787-098-8	Sequence 8, Appli
36	386	18.6	370	6	US-11-054-211-21	Sequence 21, Appl
37	386	18.6	370	6	US-11-054-211-104	Sequence 104, App
38	386	18.6	370	6	US-11-116-727-46	Sequence 46, Appl
39	385.5	18.6	370	3	US-09-799-955-2	Sequence 2, Appli
40	385.5	18.6	370	3	US-09-799-955-3	Sequence 3, Appli
41	382	18.4	376	4	US-10-369-493-6183	Sequence 6183, Ap
42	382	18.4	376	5	US-10-650-467-44	Sequence 44, Appl
43	379	18.3	481	5	US-10-489-425-68	Sequence 68, Appl
44	373.5	18.0	370	3	US-09-799-955-7	Sequence 7, Appli
45	373.5	18.0	370	4	US-10-787-098-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-10-650-467-105
; Sequence 105, Application US/10650467
; Publication No. US20050176069A1
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Geary, Timothy G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/10/650,467
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/721,870
; PRIOR FILING DATE: CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-650-467-105

Query Match 100.0%; Score 2074; DB 5; Length 397;
Best Local Similarity 100.0%; Pred. No. 1.9e-174;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MVSSAATISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MVSSAATISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF 60

Qy         61 LYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKD 120

Qy        121 WAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 WAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIV 180

Qy        181 STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM 240

Qy        241 AVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 300

Qy        301 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKIL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKIL 360
```

```
Qy        361 NSTEGSKKAGGSGLRGIQLHDLLPTSTHSDRCAGNSF 397
              |||||||||||||||||||||||||||||||||||||||
Db        361 NSTEGSKKAGGSGLRGIQLHDLLPTSTHSDRCAGNSF 397


RESULT 2
US-10-650-467-40
; Sequence 40, Application US/10650467
; Publication No. US20050176069A1
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Geary, Timothy G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 28341/6223
;  CURRENT APPLICATION NUMBER: US/10/650,467
;  CURRENT FILING DATE:  2003-08-28
;  PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/721,870
;  PRIOR FILING DATE: CURRENT FILING DATE:  2000-11-24
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
;   LENGTH: 499
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-650-467-40

  Query Match             100.0%;  Score 2074;  DB 5;  Length 499;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-174;
  Matches  397;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MVSSAATISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        103 MVSSAATISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF 162

Qy         61 LYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 LYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKD 222

Qy        121 WAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        223 WAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIV 282

Qy        181 STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM 342

Qy        241 AVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 AVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 402

Qy        301 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKIL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKIL 462

Qy        361 NSTEGSKKAGGSGLRGIQLHDLLPTSTHSDRCAGNSF 397
              |||||||||||||||||||||||||||||||||||||
Db        463 NSTEGSKKAGGSGLRGIQLHDLLPTSTHSDRCAGNSF 499


RESULT 3
US-10-650-467-107
; Sequence 107, Application US/10650467
; Publication No. US20050176069A1
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Geary, Timothy G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 28341/6223
;  CURRENT APPLICATION NUMBER: US/10/650,467
;  CURRENT FILING DATE:  2003-08-28
;  PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/721,870
;  PRIOR FILING DATE: CURRENT FILING DATE:  2000-11-24
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
;   LENGTH: 433
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-650-467-107

  Query Match             91.6%;  Score 1899;  DB 5;  Length 433;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-159;
  Matches  364;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MVSSAATISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MVSSAATISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF 60

Qy         61 LYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKD 120

Qy        121 WAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 WAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIV 180

Qy        181 STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM 240

Qy        241 AVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 300

Qy        301 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKIL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKIL 360

Qy        361 NSTE 364
              ||||
Db        361 NSTE 364


RESULT 4
US-10-650-467-16
; Sequence 16, Application US/10650467
; Publication No. US20050176069A1
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Geary, Timothy G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 28341/6223
;  CURRENT APPLICATION NUMBER: US/10/650,467
;  CURRENT FILING DATE:  2003-08-28
;  PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/721,870
;  PRIOR FILING DATE: CURRENT FILING DATE:  2000-11-24
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 450
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-650-467-16

  Query Match             29.3%;  Score 607.5;  DB 5;  Length 450;
  Best Local Similarity   35.3%;  Pred. No. 6.3e-45;
  Matches  119;  Conservative   76;  Mismatches  111;  Indels   31;  Gaps    7;

Qy         33 CIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNV 92
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Db          9 CIDVNAIL--QQFNDWTVLFEVRLGYSVLYFLILIIGLVGNGLLITSILMRKKL-SVANI 65

Qy         93 FLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLD 152

Db         66 FLINLAVSDLLLCITAVPITPVLAFMKRWIFGIIMCKLVPTCQAFSVLISSWSLCYIAID 125

Qy        153 KFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDGSFYVQPGET------ 206

Db        126 RYRSIVTPLREPWSDRHARWLLMFTWVVAFLASYPL----------YYSQNLKTMVIENV 175

Qy        207 PYCGHFCDEANWQSENSRKI-YGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQF 265

Db        176 TLCGDFCGEFNWQSDEISKLTYTTSLLIIQLIIPAIIMSFCYLMILQKVQTDWLVDEGSM 235

Qy        266 CQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEW-------- 317

Db        236 ---LTAAQQAQTAVRKRRVMYVLILMVIVFMACWFPLSAVNLFRDLGMRFEFCQTVYKVL 292

Qy        318 LKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRS 354

Db        293 MMDQMYFKLLNVHVIAMTSIVWNPVLYFWMSKRHRRA 329
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RESULT 5
US-10-369-493-6608
; Sequence 6608, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6608
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6608

Query Match 29.3%; Score 607.5; DB 4; Length 539;
Best Local Similarity 35.3%; Pred. No. 7.8e-45;
Matches 119; Conservative 76; Mismatches 111; Indels 31; Gaps 7;

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Qy         33 CIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNV 92

Db          9 CIDVNAIL--QQFNDWTVLFEVRLGYSVLYFLILIIGLVGNGLLITSILMRKKL-SVANI 65

Qy         93 FLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLD 152

Db         66 FLINLAVSDLLLCITAVPITPVLAFMKRWIFGIIMCKLVPTCQAFSVLISSWSLCYIAID 125

Qy        153 KFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDGSFYVQPGET------ 206

Db        126 RYRSIVTPLREPWSDRHARWLLMFTWVVAFLASYPL----------YYSQNLKTMVIENV 175

Qy        207 PYCGHFCDEANWQSENSRKI-YGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQF 265

Db        176 TLCGDFCGEFNWQSDEISKLTYTTSLLIIQLIIPAIIMSFCYLMILQKVQTDWLVDEGSM 235

Qy        266 CQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEW-------- 317

Db        236 ---LTAAQQAQTAVRKRRVMYVLILMVIVFMACWFPLSAVNLFRDLGMRFEFCQTVYKVL 292

Qy        318 LKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRS 354

Db        293 MMDQMYFKLLNVHVIAMTSIVWNPVLYFWMSKRHRRA 329
```

RESULT 6
US-09-804-551B-8
; Sequence 8, Application US/09804551B
; Patent No. US20020056151A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Receptors for peptides from insects
; FILE REFERENCE: Le A 34 394
; CURRENT APPLICATION NUMBER: US/09/804,551B
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: DE 100 13 618.4
; PRIOR FILING DATE: 2000-03-18
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-804-551B-8

Query Match 25.5%; Score 529; DB 3; Length 518;
Best Local Similarity 30.5%; Pred. No. 6.4e-38;
Matches 136; Conservative 76; Mismatches 154; Indels 80; Gaps 12;

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Qy          6 ATISTISTTTTPST---------ISNVITSHSNNGSCIQIAEAIAAQGID---DITVDFY 53

Db          2 ANLSWLSTITTTSSSISTSQLPLVSTTNWSLTSPGTTSAILADVAASDEDRSGGIIHNQF 61

Qy         54 IRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTP 113

Db         62 VQIFFYVLYATVFVLGVFGNVLVCYVVLRNRAMQTVTNIFITNLALSDILLCVLAVPFTP 121

Qy        114 WYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAI 173

Db        122 LYTFMGRWAFGRSLCHLVSFAQGCSIYISTLTLTSIAIDRYFVIIYPFHPRMKLSTCIGI 181

Qy        174 TFLIWIVSTLINLPYLMSFE---------------------HVDGSFYVQPG-------- 204

Db        182 IVSIWVIALLATVPYGMYMKMTNELVNGTQTGNETLVEATLMLNGSFVAQGSGFIEAPDS 241

Qy        205 ------------------ETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYC 246

Db        242 TSATQAYMQVMTAGSTGPEMPYVRVYCEE-NWPSEQYRKVFGAITTTLQFVLPFFIISIC 300

Qy        247 YFKILQKVSKDMIIQNAQFCQSLTQKQRSDA-TSRKKKVNYILIAMVVTFIGCWLPLTLL 305

Db        301 YVWISVKLN-----QRARAKPGSKSSRREEADRDRKKRTNRMLIAMVAVFGLSWLPINVV 355

Qy        306 NLVKDF-KKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLT---RKQKRSGL----- 356

Db        356 NIFDDFDDKSNEWRFYILFFFV--AHSIAMSSTCYNPFLYAWLNENFRKEFKHVLPCFNP 413

Qy        357 --SKILNSTEGSKKAGGSGLRGIQLH 380

Db        414 SNNNIIINITRGYNRSDRNTC-GPRLH 438
```

RESULT 7
US-10-283-423-2
; Sequence 2, Application US/10283423
; Publication No. US20030162223A1
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Metho
; TITLE OF INVENTION: Related To The Same
; FILE REFERENCE: PHRM0002-102

```
;    Application Project
;    -------------------
;  CURRENT APPLICATION NUMBER: US/10/283,423
;  CURRENT FILING DATE:  2002-10-30
;    Earlier Applications
;    --------------------
;  PRIOR APPLICATION NUMBER: PriorAppNumber : 09/693,746
;  PRIOR FILING DATE: PriorFilingDate : 2000-10-20
;  PRIOR APPLICATION NUMBER: PriorAppNumber : 09/425,676
;  PRIOR FILING DATE: PriorFilingDate : 1999-10-22
;  NUMBER OF SEQ ID NOS: 187
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: D. melanogaster
US-10-283-423-2

  Query Match             25.5%;  Score 529;  DB 4;  Length 600;
  Best Local Similarity   30.5%;  Pred. No. 7.6e-38;
  Matches  136;  Conservative   76;  Mismatches  154;  Indels   80;  Gaps   12;

Qy          6 ATISTISTTTTPST---------ISNVITSHSNNGSCIQIAEAIAAQGID---DITVDFY 53
              | :| :|| || |:         :|    | :: |:   |   :||   |   | : :
Db          2 ANLSWLSTITTTSSSISTSQLPLVSTTNWSLTSPGTTSAILADVAASDEDRSGGIIHNQF 61

Qy         54 IRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTP 113
              ::  |  ||  :||||:|||  | : | ||: :|:  |:|: ||  :|::|   |:| ||
Db         62 VQIFFYVLYATVFVLGVFGNVLVCYVVLRNRAMQTVTNIFITNLALSDILLCVLAVPFTP 121

Qy        114 WYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAI 173
               |      ||||  :|||  :  ||:::: :||:|::|::  |  |    : :  : |
Db        122 LYTFMGRWAFGRSLCHLVSFAQGCSIYISTLTLTSIAIDRYFVIIYPFHPRMKLSTCIGI 181

Qy        174 TFLIWIVSTLINLPYLMSFE--------------------HVDGSFYVQPG-------- 204
              ||::: |  :|| |  :                     ::||| |
Db        182 IVSIWVIALLATVPYGMYMKMTNELVNGTQTGNETLVEATLMLNGSFVAQGSGFIEAPDS 241

Qy        205 ------------------ETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYC 246
                             | ||   :|:| || ||  ||::|     ||||:|  :|: |
Db        242 TSATQAYMQVMTAGSTGPEMPYVRVYCEE-NWPSEQYRKVFGAITTTLQFVLPFFIISIC 300

Qy        247 YFKILQKVSKDMIIQNAQFCQSLTQKQRSDA-TSRKKKVNYILIAMVVTFIGCWLPLTLL 305
              |  |  |::     | |:         :| :|   |||: | :|||||  |   |||: ::
Db        301 YVWISVKLN-----QRARAKPGSKSSRREEADRDRKKRTNRMLIAMVAVFGLSWLPINVV 355

Qy        306 NLVKDF-KKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLT---RKQKRSGL----- 356
              |:  ||  |  ||     ||:   || ||||   :|| |: ||    ||: :  |
Db        356 NIFDDFDDKSNEWRFYILFFFV--AHSIAMSSTCYNPFLYAWLNENFRKEFKHVLPCFNP 413

Qy        357 --SKILNSTEGSKKAGGSGLRGIQLH 380
                : |:| | |  ::  :   | :||
Db        414 SNNNIIINITRGYNRSDRNTC-GPRLH 438


RESULT 8
US-10-213-821-2
; Sequence 2, Application US/10213821
; Publication No. US20030180297A1
; GENERAL INFORMATION:
;  APPLICANT: Pharmacia & Upjphn
;  APPLICANT:  Lowery, David E.
;  APPLICANT:  Smith, Valdin G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
;  TITLE OF INVENTION:  Related To The Same
;  FILE REFERENCE: 6297.2cp
;  CURRENT APPLICATION NUMBER: US/10/213,821
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 09/693,746
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 09/425,676
;  PRIOR FILING DATE: 1999-10-22
;  NUMBER OF SEQ ID NOS: 185
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: D. melanogaster
US-10-213-821-2

  Query Match             25.5%;  Score 529;  DB 4;  Length 600;
  Best Local Similarity   30.5%;  Pred. No. 7.6e-38;
  Matches  136;  Conservative   76;  Mismatches  154;  Indels   80;  Gaps   12;

Qy          6 ATISTISTTTTPST---------ISNVITSHSNNGSCIQIAEAIAAQGID---DITVDFY 53
              | :| :|| || |:         :|    | :: |:   |   :||   |   | : :
Db          2 ANLSWLSTITTTSSSISTSQLPLVSTTNWSLTSPGTTSAILADVAASDEDRSGGIIHNQF 61

Qy         54 IRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTP 113
              ::  |  ||  :||||:|||  | : | ||: :|:  |:|: ||  :|::|   |:| ||
Db         62 VQIFFYVLYATVFVLGVFGNVLVCYVVLRNRAMQTVTNIFITNLALSDILLCVLAVPFTP 121

Qy        114 WYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAI 173
               |      ||||  :|||  :  ||:::: :||:|::|::  |  |    : :  : |
Db        122 LYTFMGRWAFGRSLCHLVSFAQGCSIYISTLTLTSIAIDRYFVIIYPFHPRMKLSTCIGI 181

Qy        174 TFLIWIVSTLINLPYLMSFE--------------------HVDGSFYVQPG-------- 204
              ||::: |  :|| |  :                     ::||| |
Db        182 IVSIWVIALLATVPYGMYMKMTNELVNGTQTGNETLVEATLMLNGSFVAQGSGFIEAPDS 241

Qy        205 ------------------ETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYC 246
                             | ||   :|:| || ||  ||::|     ||||:|  :|: |
Db        242 TSATQAYMQVMTAGSTGPEMPYVRVYCEE-NWPSEQYRKVFGAITTTLQFVLPFFIISIC 300

Qy        247 YFKILQKVSKDMIIQNAQFCQSLTQKQRSDA-TSRKKKVNYILIAMVVTFIGCWLPLTLL 305
              |  |  |::     | |:         :| :|   |||: | :|||||  |   |||: ::
Db        301 YVWISVKLN-----QRARAKPGSKSSRREEADRDRKKRTNRMLIAMVAVFGLSWLPINVV 355

Qy        306 NLVKDF-KKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLT---RKQKRSGL----- 356
              |:  ||  |  ||     ||:   || ||||   :|| |: ||    ||: :  |
Db        356 NIFDDFDDKSNEWRFYILFFFV--AHSIAMSSTCYNPFLYAWLNENFRKEFKHVLPCFNP 413

Qy        357 --SKILNSTEGSKKAGGSGLRGIQLH 380
                : |:| | |  ::  :   | :||
Db        414 SNNNIIINITRGYNRSDRNTC-GPRLH 438


RESULT 9
US-10-736-048-2
; Sequence 2, Application US/10736048
; Publication No. US20040121956A1
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Smith, Valdin G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
;  TITLE OF INVENTION:  Related To The Same
;  FILE REFERENCE: 6297.1cp
;  CURRENT APPLICATION NUMBER: US/10/736,048
;  CURRENT FILING DATE:  2003-12-15
;  PRIOR APPLICATION NUMBER: US/09/693,746
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 09/425,676
;  PRIOR FILING DATE: 1999-10-22
;  NUMBER OF SEQ ID NOS: 168
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: D. melanogaster
US-10-736-048-2

  Query Match             25.5%;  Score 529;  DB 4;  Length 600;
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  Best Local Similarity   30.5%;  Pred. No. 7.6e-38;
  Matches  136;  Conservative   76;  Mismatches  154;  Indels   80;  Gaps   12;

Qy          6 ATISTISTTTTPST---------ISNVITSHSNNGSCIQIAEAIAAQGID---DITVDFY 53
              | :| :|| || |:          :|    | :: |:   |   :||   |    |  : :
Db          2 ANLSWLSTITTTSSSISTSQLPLVSTTNWSLTSPGTTSAILADVAASDEDRSGGIIHNQF 61

Qy         54 IRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTP 113
              ::  |  ||  :||||:|||  | : | ||: :|:  |:|: ||  :|::|   |:| ||
Db         62 VQIFFYVLYATVFVLGVFGNVLVCYVVLRNRAMQTVTNIFITNLALSDILLCVLAVPFTP 121

Qy        114 WYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAI 173
              |    |||| :|||| :|||:|::|:|::   |  |    : :  : |
Db        122 LYTFMGRWAFGRSLCHLVSFAQGCSIYISTLTLTSIAIDRYFVIIYPFHPRMKLSTCIGI 181

Qy        174 TFLIWIVSTLINLPYLMSFE--------------------HVDGSFYVQPG-------- 204
                ||::: |  :|| |  :                    ::|||  |
Db        182 IVSIWVIALLATVPYGMYMKMTNELVNGTQTGNETLVEATLMLNGSFVAQGSGFIEAPDS 241

Qy        205 ------------------ETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYC 246
                                 | ||   :|:| || ||  ||::|     ||||:|  :|: |
Db        242 TSATQAYMQVMTAGSTGPEMPYVRVYCEE-NWPSEQYRKVFGAITTTLQFVLPFFIISIC 300

Qy        247 YFKILQKVSKDMIIQNAQFCQSLTQKQRSDA-TSRKKKVNYILIAMVVTFIGCWLPLTLL 305
              |  |  |::     | |:         :| :|   |||: | :|||||  |   |||: ::
Db        301 YVWISVKLN-----QRARAKPGSKSSRREEADRDRKKRTNRMLIAMVAVFGLSWLPINVV 355

Qy        306 NLVKDF-KKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLT---RKQKRSGL----- 356
              |:  ||  |  ||     ||:   || ||||   :|| |: ||    ||: :  |
Db        356 NIFDDFDDKSNEWRFYILFFFV--AHSIAMSSTCYNPFLYAWLNENFRKEFKHVLPCFNP 413

Qy        357 --SKILNSTEGSKKAGGSGLRGIQLH 380
                : |:| | |  ::  :   | :||
Db        414 SNNNIIINITRGYNRSDRNTC-GPRLH 438


RESULT 10
US-10-489-425-62
; Sequence 62, Application US/10489425
; Publication No. US20040248791A1
; GENERAL INFORMATION:
;  APPLICANT: Syngenta Participations AG
;  APPLICANT:  Spana, Eric
;  APPLICANT:  Kamdar, Kim
;  APPLICANT:  Stam, Lynn
;  APPLICANT:  Valentine, Scott
;  APPLICANT:  Griswald, Charles M
;  TITLE OF INVENTION: Insect G Protein-Coupled Receptor Genes and Uses thereof
;  FILE REFERENCE: 60134WOPCT
;  CURRENT APPLICATION NUMBER: US/10/489,425
;  CURRENT FILING DATE:  2004-03-08
;  PRIOR APPLICATION NUMBER: 60/341,512
;  PRIOR FILING DATE: 2001-12-18
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-10-489-425-62

  Query Match             25.5%;  Score 529;  DB 5;  Length 600;
  Best Local Similarity   30.5%;  Pred. No. 7.6e-38;
  Matches  136;  Conservative   76;  Mismatches  154;  Indels   80;  Gaps   12;

Qy          6 ATISTISTTTTPST---------ISNVITSHSNNGSCIQIAEAIAAQGID---DITVDFY 53
              | :| :|| || |:          :|    | :: |:   |   :||   |    |  : :
Db          2 ANLSWLSTITTTSSSISTSQLPLVSTTNWSLTSPGTTSAILADVAASDEDRSGGIIHNQF 61

Qy         54 IRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTP 113
              ::  |  ||  :||||:|||  | : | ||: :|:  |:|: ||  :|::|   |:| ||
Db         62 VQIFFYVLYATVFVLGVFGNVLVCYVVLRNRAMQTVTNIFITNLALSDILLCVLAVPFTP 121

Qy        114 WYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAI 173
              |    |||| :|||| :|||:|::|:|::   |  |    : :  : |
Db        122 LYTFMGRWAFGRSLCHLVSFAQGCSIYISTLTLTSIAIDRYFVIIYPFHPRMKLSTCIGI 181

Qy        174 TFLIWIVSTLINLPYLMSFE--------------------HVDGSFYVQPG-------- 204
                ||::: |  :|| |  :                    ::|||  |
Db        182 IVSIWVIALLATVPYGMYMKMTNELVNGTQTGNETLVEATLMLNGSFVAQGSGFIEAPDS 241

Qy        205 ------------------ETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYC 246
                                 | ||   :|:| || ||  ||::|     ||||:|  :|: |
Db        242 TSATQAYMQVMTAGSTGPEMPYVRVYCEE-NWPSEQYRKVFGAITTTLQFVLPFFIISIC 300

Qy        247 YFKILQKVSKDMIIQNAQFCQSLTQKQRSDA-TSRKKKVNYILIAMVVTFIGCWLPLTLL 305
              |  |  |::     | |:         :| :|   |||: | :|||||  |   |||: ::
Db        301 YVWISVKLN-----QRARAKPGSKSSRREEADRDRKKRTNRMLIAMVAVFGLSWLPINVV 355

Qy        306 NLVKDF-KKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLT---RKQKRSGL----- 356
              |:  ||  |  ||     ||:   || ||||   :|| |: ||    ||: :  |
Db        356 NIFDDFDDKSNEWRFYILFFFV--AHSIAMSSTCYNPFLYAWLNENFRKEFKHVLPCFNP 413

Qy        357 --SKILNSTEGSKKAGGSGLRGIQLH 380
                : |:| | |  ::  :   | :||
Db        414 SNNNIIINITRGYNRSDRNTC-GPRLH 438


RESULT 11
US-11-097-143-41472
; Sequence 41472, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
;  APPLICANT: Venter, J. Craig
;  APPLICANT:  et al.
;  TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
;  TITLE OF INVENTION:  ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
;  TITLE OF INVENTION:  DROSOPHILA GENES.
;  FILE REFERENCE: CL000728
;  CURRENT APPLICATION NUMBER: US/11/097,143
;  CURRENT FILING DATE:  2005-04-04
;  PRIOR APPLICATION NUMBER: 60/157,832
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: 60/160,191
;  PRIOR FILING DATE: 1999-10-19
;  PRIOR APPLICATION NUMBER: 60/161,932
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: 60/164,769
;  PRIOR FILING DATE: 1999-11-12
;  PRIOR APPLICATION NUMBER: 60/173,383
;  PRIOR FILING DATE: 1999-12-28
;  PRIOR APPLICATION NUMBER: 60/175,693
;  PRIOR FILING DATE: 2000-01-12
;  PRIOR APPLICATION NUMBER: 60/184,831
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: 60/191,637
;  PRIOR FILING DATE: 2000-03-23
;  NUMBER OF SEQ ID NOS: 43008
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41472
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: DROSOPHILA
US-11-097-143-41472

  Query Match             25.5%;  Score 529;  DB 6;  Length 600;
  Best Local Similarity   30.5%;  Pred. No. 7.6e-38;
  Matches  136;  Conservative   76;  Mismatches  154;  Indels   80;  Gaps   12;

Qy          6 ATISTISTTTTPST---------ISNVITSHSNNGSCIQIAEAIAAQGID---DITVDFY 53
              | :| :|| || |:          :|    | :: |:   |   :||   |    |  : :
Db          2 ANLSWLSTITTTSSSISTSQLPLVSTTNWSLTSPGTTSAILADVAASDEDRSGGIIHNQF 61

Qy         54 IRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTP 113
              ::  |  ||  :||||:|||  | : | ||: :|:  |:|: ||  :|::|   |:| ||
Db         62 VQIFFYVLYATVFVLGVFGNVLVCYVVLRNRAMQTVTNIFITNLALSDILLCVLAVPFTP 121
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Qy        114 WYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAI 173
Db        122 LYTFMGRWAFGRSLCHLVSFAQGCSIYISTLTLTSIAIDRYFVIIYPFHPRMKLSTCIGI 181

Qy        174 TFLIWIVSTLINLPYLMSFE--------------------HVDGSFYVQPG-------- 204
Db        182 IVSIWVIALLATVPYGMYMKMTNELVNGTQTGNETLVEATLMLNGSFVAQGSGFIEAPDS 241

Qy        205 ------------------ETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYC 246
Db        242 TSATQAYMQVMTAGSTGPEMPYVRVYCEE-NWPSEQYRKVFGAITTTLQFVLPFFIISIC 300

Qy        247 YFKILQKVSKDMIIQNAQFCQSLTQKQRSDA-TSRKKKVNYILIAMVVTFIGCWLPLTLL 305
Db        301 YVWISVKLN-----QRARAKPGSKSSRREEADRDRKKRTNRMLIAMVAVFGLSWLPINVV 355

Qy        306 NLVKDF-KKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLT---RKQKRSGL----- 356
Db        356 NIFDDFDDKSNEWRFYILFPFV--AHSIAMSSTCYNPFLYAWLNENFRKEFKHVLPCFNP 413

Qy        357 --SKILNSTEGSKKAGGSGLRGIQLH 380
Db        414 SNNNIINITRGYNRSDRNTC-GPRLH 438
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RESULT 12
US-10-650-467-22
; Sequence 22, Application US/10650467
; Publication No. US20050176069A1
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Geary, Timothy G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/10/650,467
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/721,870
; PRIOR FILING DATE: CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-650-467-22

Query Match 24.9%; Score 515.5; DB 5; Length 376;
Best Local Similarity 30.3%; Pred. No. 6.7e-37;
Matches 119; Conservative 78; Mismatches 131; Indels 65; Gaps 11;

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Qy         29 NNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQS 88
Db          2 NGSDCLNLNSELWLYR-EDLSSRWYIMLVFAFLYLIIIAAGIIGNSCVILAITRNKSLQT 60

Qy         89 ARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTA 148
Db         61 VPNLFILSLSCSDIVVCCTSATITPITAFKKEWIFGEALCRIAPFIAGISLCFSTFTLTA 120

Qy        149 ISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDGSFYVQPGETPY 208
Db        121 ISIDRYILIRFPMRKPITHYQAVGVIAIICAFAATITSPIM--FKQKLGEF------ENF 172

Qy        209 CGHFCDEANW-QSENSRKIYGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQFCQ 267
Db        173 CGQYCTE-NWGANESQRKIYGAALMFLQLVIPLTIIIISYTAISLKIGQSMILKGA---- 227

Qy        268 SLTQKQRSD------------ATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEP 315
Db        228 ---KKQKTDNWEMELSDQQRIAVKRRQRTNRMLIGMVVAFACSWIWSVTFNILRDYEYLP 284

Qy        316 EWLKRQPFFWAINAHVIAMSLVVWNPLLF----------------FWLTRKQKRSG--LS 357
Db        285 ELIKTQEYIFGIATHCIAMTSTVWNPLLYAVLNLQLRAAFIDLMPHWLRRHLNLEGDNSS 344

Qy        358 KILN------STEGSKKAGGSGLRGIQLHDLLP 384
Db        345 PLLNHPTMTITNKPSKQ-----------HTLIP 366
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RESULT 13
US-10-369-493-6944
; Sequence 6944, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6944
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6944

Query Match 24.8%; Score 514; DB 4; Length 374;
Best Local Similarity 31.3%; Pred. No. 9.1e-37;
Matches 114; Conservative 74; Mismatches 128; Indels 48; Gaps 9;

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Qy         29 NNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQS 88
Db          2 NGSDCLNLNSELWLYR-EDLSSRWYIMLVFAFLYLIIIAAGIIGNSCVILAITRNKSLQT 60

Qy         89 ARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTA 148
Db         61 VPNLFILSLSCSDIVVCCTSATITPITAFKKEWIFGEALCRIAPFIAGISLCFSTFTLTA 120

Qy        149 ISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDGSFYVQPGETPY 208
Db        121 ISIDRYILIRFPMRKPITHYQAVGVIAIICAFAATITSPIM--FKQKLGEF------ENF 172

Qy        209 CGHFCDEANW-QSENSRKIYGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQFCQ 267
Db        173 CGQYCTE-NWGANESQRKIYGAALMFLQLVIPLTIIIISYTAISLKIGQSMILKGA---- 227

Qy        268 SLTQKQRSD------------ATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEP 315
Db        228 ---KKQKTDNWEMELSDQQRIAVKRRQRTNRMLIGMVVAFACSWIWSVTFNILRDYEYLP 284

Qy        316 EWLKRQPFFWAINAHVIAMSLVVWNPLLF----------------FWLTRKQKRSG--LS 357
Db        285 ELIKTQEYIFGIATHCIAMTSTVWNPLLYAVLNLQLRAAFIDLMPHWLRRHLNLEGDNSS 344

Qy        358 KILN 361
Db        345 PLLN 348
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RESULT 14
US-10-369-493-6769
; Sequence 6769, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6769
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6769

Query Match 23.4%; Score 485.5; DB 4; Length 457;
Best Local Similarity 30.8%; Pred. No. 3.8e-34;
Matches 117; Conservative 69; Mismatches 117; Indels 77; Gaps 10;

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Qy         58 FTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAM 117
              |  :| ||| ||:|||  :::    :| | | :|:|:|||  :| ::   ::|:||   :
Db         29 FLTVYLFLFFLGLFGNVTLIYVTCSHKALLSVQNIFILNLAASDCMMCILSLPITPITNV 88

Qy        118 TKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLI 177
               |:| ||:::|||:|     |:|| ::|| ||:||::: :  |   |:| | |   | |:
Db         89 YKNWYFGNLLCHLIPCIQGISIFVCTFSLGAIALDRYILVVRPHSTPLSQRGAFLTTVLL 148

Qy        178 WIVSTLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFV 237
              ||:| :: ||| : : :: :      |   ||:|| |  |:|  ||: |   ||| |||
Db        149 WILSFVVTLPYAFNMQMIEYT------EERICGYFCTE-KWESAKSRRAYTMIVMLAQFV 201

Qy        238 VPMAVITYCYFKILQKVSK-------DMIIQNA--------------QFCQSLT------ 270
              || ||: :||  |:  :||        |: : :               |:  |
Db        202 VPFAVMAFCYANIVSVLSKRAQTKIRKMVERTSALESSCAFPSHGLEQYENELNEFLDKQ 261

Qy        271 QKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEWLKRQPFF------ 324
              :|::     : ::   ||: ||| |   |||  :::|: ::        | ||
Db        262 EKEKQRVVLQNRRTTSILVTMVVWFGITWLPHNVISLIIEYD------DTQSFFRLYGRD 315

Qy        325 -----WAIN--AHVIAMSLVVWNPLLFFWL----------TRKQKRSGLSKILNST---- 363
                  : :|   | ||||  | ||:|: ||          |    |    :|:| |
Db        316 DYDISYLLNLFTHSIAMSNNVLNPVLYAWLNPSFRQLVIKTYFGDRRKSDRIINQTSVYK 375

Qy        364 ----------EGSKKAGGSG 373
                       |  | || |
Db        376 TKIVHDTKHLNGRAKIGGGG 395
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RESULT 15
US-10-650-467-26
; Sequence 26, Application US/10650467
; Publication No. US20050176069A1
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Geary, Timothy G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/10/650,467
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/721,870
; PRIOR FILING DATE: CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-650-467-26

Query Match 23.4%; Score 485.5; DB 5; Length 457;
Best Local Similarity 30.8%; Pred. No. 3.8e-34;
Matches 117; Conservative 69; Mismatches 117; Indels 77; Gaps 10;

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Qy         58 FTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAM 117
              |  :| ||| ||:|||  :::    :| | | :|:|:|||  :| ::   ::|:||   :
Db         29 FLTVYLFLFFLGLFGNVTLIYVTCSHKALLSVQNIFILNLAASDCMMCILSLPITPITNV 88

Qy        118 TKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLI 177
               |:| ||:::|||:|     |:|| ::|| ||:||::: :  |   |:| | |   | |:
Db         89 YKNWYFGNLLCHLIPCIQGISIFVCTFSLGAIALDRYILVVRPHSTPLSQRGAFLTTVLL 148

Qy        178 WIVSTLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFV 237
              ||:| :: ||| : : :: :      |   ||:|| |  |:|  ||: |   ||| |||
Db        149 WILSFVVTLPYAFNMQMIEYT------EERICGYFCTE-KWESAKSRRAYTMIVMLAQFV 201

Qy        238 VPMAVITYCYFKILQKVSK-------DMIIQNA--------------QFCQSLT------ 270
              || ||: :||  |:  :||        |: : :               |:  |
Db        202 VPFAVMAFCYANIVSVLSKRAQTKIRKMVERTSALESSCAFPSHGLEQYENELNEFLDKQ 261

Qy        271 QKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEWLKRQPFF------ 324
              :|::     : ::   ||: ||| |   |||  :::|: ::        | ||
Db        262 EKEKQRVVLQNRRTTSILVTMVVWFGITWLPHNVISLIIEYD------DTQSFFRLYGRD 315

Qy        325 -----WAIN--AHVIAMSLVVWNPLLFFWL----------TRKQKRSGLSKILNST---- 363
                  : :|   | ||||  | ||:|: ||          |    |    :|:| |
Db        316 DYDISYLLNLFTHSIAMSNNVLNPVLYAWLNPSFRQLVIKTYFGDRRKSDRIINQTSVYK 375

Qy        364 ----------EGSKKAGGSG 373
                       |  | || |
Db        376 TKIVHDTKHLNGRAKIGGGG 395
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Search completed: May 8, 2006, 09:38:01
Job time : 168 secs

GenCore version 5.1.8

OM protein - protein search, using sw model

Run on: May 8, 2006, 09:35:22 ; Search time 28 Seconds
(without alignments)
656.251 Million cell updates/sec

Title: US-10-650-467-105
Perfect score: 2074
Sequence: 1 MVSSAATISTISTTTTPSTI.....QLHDLLPTSTHSDRCAGNSF 397

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep1:*
2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
7: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep1:*
8: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
9: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep1:*
10: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
11: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep1:*
12: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	348.5	16.8	384	9	US-10-987-856-15	Sequence 15, Appl
2	346.5	16.7	384	11	US-11-080-991-26	Sequence 26, Appl
3	346.5	16.7	384	11	US-11-183-615-4	Sequence 4, Appli
4	324	15.6	381	9	US-10-987-856-16	Sequence 16, Appl
5	314	15.1	375	9	US-10-987-856-17	Sequence 17, Appl
6	304	14.7	420	9	US-10-992-577-6	Sequence 6, Appli
7	304	14.7	522	9	US-10-510-018-2	Sequence 2, Appli
8	286.5	13.8	254	9	US-10-055-877-248	Sequence 248, App
9	286.5	13.8	254	9	US-10-055-877-327	Sequence 327, App
10	286.5	13.8	254	9	US-10-055-877-340	Sequence 340, App
11	286.5	13.8	254	9	US-10-877-346-83	Sequence 83, Appl
12	285.5	13.8	430	9	US-10-992-577-8	Sequence 8, Appli
13	285.5	13.8	430	9	US-10-508-892-2	Sequence 2, Appli
14	285.5	13.8	430	11	US-11-223-294-54	Sequence 54, Appl
15	285.5	13.8	432	9	US-10-992-577-2	Sequence 2, Appli
16	285.5	13.8	432	11	US-11-223-294-37	Sequence 37, Appl
17	284	13.7	417	9	US-10-992-577-44	Sequence 44, Appl
18	277	13.4	394	11	US-11-183-615-17	Sequence 17, Appl
19	274.5	13.2	388	9	US-10-995-561-838	Sequence 838, App
20	274.5	13.2	389	9	US-10-995-561-837	Sequence 837, App
21	271.5	13.1	393	10	US-11-304-129-40	Sequence 40, Appl
22	267	12.9	393	9	US-10-504-588-8	Sequence 8, Appli
23	267	12.9	393	10	US-11-304-129-48	Sequence 48, Appl
24	266.5	12.8	400	11	US-11-127-877-55	Sequence 55, Appl
25	262.5	12.7	259	9	US-10-055-877-225	Sequence 225, App
26	262.5	12.7	259	9	US-10-055-877-237	Sequence 237, App
27	262.5	12.7	259	11	US-11-206-587-27	Sequence 27, Appl
28	262.5	12.7	259	11	US-11-206-587-29	Sequence 29, Appl
29	261.5	12.6	359	8	US-10-511-937-2990	Sequence 2990, Ap
30	261	12.6	381	10	US-11-304-129-49	Sequence 49, Appl
31	261	12.6	384	9	US-10-504-588-2	Sequence 2, Appli
32	261	12.6	384	10	US-11-304-129-36	Sequence 36, Appl
33	261	12.6	384	11	US-11-073-420-7	Sequence 7, Appli
34	260.5	12.6	380	11	US-11-210-139-17	Sequence 17, Appl
35	260.5	12.6	442	11	US-11-100-640-34	Sequence 34, Appl
36	260	12.5	384	11	US-11-073-420-4	Sequence 4, Appli
37	257.5	12.4	359	9	US-10-995-561-712	Sequence 712, App
38	257.5	12.4	359	9	US-10-995-561-716	Sequence 716, App
39	257.5	12.4	359	11	US-11-127-877-65	Sequence 65, Appl
40	257.5	12.4	388	9	US-10-995-561-713	Sequence 713, App
41	257.5	12.4	394	9	US-10-995-561-714	Sequence 714, App
42	257.5	12.4	394	9	US-10-995-561-715	Sequence 715, App
43	256	12.3	384	11	US-11-073-420-2	Sequence 2, Appli
44	256	12.3	384	11	US-11-073-420-8	Sequence 8, Appli
45	254.5	12.3	359	9	US-10-876-787-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-987-856-15
; Sequence 15, Application US/10987856
; Publication No. US20060014242A1
; GENERAL INFORMATION:
; APPLICANT: GERALD, CHRISTOPHE P.G.
; APPLICANT: WEINSHANK, RICHARD L
; APPLICANT: WALKER, MARY W
; APPLICANT: BRANCHEK, THERESA
; TITLE OF INVENTION: MODIFYING FEEDING BEHAVIOR, COMPOUNDS USEFUL IN SUCH METHODS, AN
; TITLE OF INVENTION: ENCODING A HYPOTHALAMIC ATYPICAL NEUROPEPTIDE Y/PEPTIDE YY RECE
; FILE REFERENCE: 1795/46166BZA
; CURRENT APPLICATION NUMBER: US/10/987,856
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/09/962,646
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/200,673
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 08/566,096
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 08/349,025
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-987-856-15

Query Match 16.8%; Score 348.5; DB 9; Length 384;
Best Local Similarity 25.7%; Pred. No. 1.5e-23;
Matches 88; Conservative 79; Mismatches 153; Indels 23; Gaps 6;

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Qy          18 STISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVL 77
               ||: : : :|| : :  :    : |   ||  :   :        || : :||: ||  ::
Db           3 STLFSQVENHSVHSNFSEKNAQLLAPENDDCHLPLAMIFTLALAYGAVIILGVSGNLALI 62

Qy          78 WAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSC 137
                 : : | :::  |: ::|| |:||::    :|:|  | :   | ||  || | |
Db          63 IIILKQKEMRNVTNILIVNLSFSDLLVAIMCLPLTFVYTLMDHWVFGEAMCKLNPFVQCV 122

Qy         138 SVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLM------- 190
                |: |: :||  |::::   | :|     : | |     :||:::   :||:|:
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Db        123 SITVSIFSLVLIAVERHQLIINPRGWRPNNRHAYVGIAVIWVLAVASSLPFLIYQVMTDE 182

Qy        191 SFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYCYFKI 250
              |::|    |           : | :  : |:: |  | | :::||:  |:  |  |||||
Db        183 PFQNVTLDAYKDK-------YVCFD-QFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKI 234

Qy        251 LQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKD 310
              :: :    :|    :     | ||  |   |::| :|:::|| |  ||||||: | | |
Db        235 YIRLKR----RNNMMDKMRDNKYRSSET---KRINIMLLSIVVAFAVCWLPLTIFNTVFD 287

Qy        311 FKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKR 353
              :  :          : :  |: ||     ||: : :| :  :|
Db        288 WNHQIIATCNHNLLFLL-CHLTAMISTCVNPIFYGFLNKNFQR 329


RESULT 2
US-11-080-991-26
; Sequence 26, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
;  APPLICANT: Veiby, Petter Ole
;  TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
;  TITLE OF INVENTION:  AND OVARIAN CANCER
;  FILE REFERENCE: MRI-039
;  CURRENT APPLICATION NUMBER: US/11/080,991
;  CURRENT FILING DATE:  2005-03-11
;  PRIOR APPLICATION NUMBER: US/10/176,847
;  PRIOR FILING DATE: 2002-06-21
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
;   LENGTH: 384
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-080-991-26

  Query Match             16.7%;  Score 346.5;  DB 11;  Length 384;
  Best Local Similarity   25.7%;  Pred. No. 2.2e-23;
  Matches   88;  Conservative   78;  Mismatches  154;  Indels   23;  Gaps    6;

Qy         18 STISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVL 77
              ||: : : :|| : :  :    : |   ||  :   :         || : :||: ||  ::
Db          3 STLFSQVENHSVHSNFSEKNAQLLAFENDDCHLPLAMIFTLALAYGAVIILGVSGNLALI 62

Qy         78 WAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSC 137
                : : | :::  |: ::|| |:||::    :| |  | :   | ||  || | |
Db         63 IIILKQKEMRNVTNILIVNLSFSDLLVAIMCLPFTFVYTLMDHWVFGEAMCKLNPFVQCV 122

Qy        138 SVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLM------- 190
              |: |: :||  |::::   | :|     : | |     :||:::   :||:|:
Db        123 SITVSIFSLVLIAVERHQLIINPRGWRPNNRHAYVGIAVIWVLAVASSLPFLIYQVMTDE 182

Qy        191 SFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYCYFKI 250
              |::|    |           : | :  : |:: |  | | :::||:  |:  |  |||||
Db        183 PFQNVTLDAYKDK-------YVCFD-QFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKI 234

Qy        251 LQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKD 310
              :: :    :|    :     | ||  |   |::| :|:::|| |  ||||||: | | |
Db        235 YIRLKR----RNNMMDKMRDNKYRSSET---KRINIMLLSIVVAFAVCWLPLTIFNTVFD 287

Qy        311 FKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKR 353
              :  :          : :  |: ||     ||: : :| :  :|
Db        288 WNHQIIATCNHNLLFLL-CHLTAMISTCVNPIFYGFLNKNFQR 329


RESULT 3
US-11-183-615-4
; Sequence 4, Application US/11183615
; Publication No. US20060040964A1
; GENERAL INFORMATION:
;  APPLICANT: Bakthavatchalam, Rajagopal
;  APPLICANT:  Blum, Charles  A.
;  APPLICANT:  Brielmann, Harry L.
;  APPLICANT:  Darrow, James W.
;  APPLICANT:  De Lombaert, Stephane W.
;  APPLICANT:  Hutchinson, Alan W.
;  APPLICANT:  Tran, Jennifer W.
;  APPLICANT:  Zheng, Xiaozhang W.
;  APPLICANT:  Elliott, Richard  L.
;  APPLICANT:  Hammond, Marlys L.
;  TITLE OF INVENTION: SPIRO[ISOBENZOFURAN-1,4'-PIPERIDIN]-3-ONES AND
;  TITLE OF INVENTION:  3H-SPIROISOBENZOFURAN-1,4'-PIPERIDINES
;  FILE REFERENCE: U 014539-7
;  CURRENT APPLICATION NUMBER: US/11/183,615
;  CURRENT FILING DATE:  2005-07-18
;  PRIOR APPLICATION NUMBER: US/10/410,648
;  PRIOR FILING DATE: 2003-04-09
;  PRIOR APPLICATION NUMBER: 10/013,846
;  PRIOR FILING DATE: 2001-12-11
;  PRIOR APPLICATION NUMBER: 60/254,990
;  PRIOR FILING DATE: 2000-12-12
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 384
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-11-183-615-4

  Query Match             16.7%;  Score 346.5;  DB 11;  Length 384;
  Best Local Similarity   25.7%;  Pred. No. 2.2e-23;
  Matches   88;  Conservative   78;  Mismatches  154;  Indels   23;  Gaps    6;

Qy         18 STISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVL 77
              ||: : : :|| : :  :    : |   ||  :   :         || : :||: ||  ::
Db          3 STLFSQVENHSVHSNFSEKNAQLLAFENDDCHLPLAMIFTLALAYGAVIILGVSGNLALI 62

Qy         78 WAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSC 137
                : : | :::  |: ::|| |:||::    :| |  | :   | ||  || | |
Db         63 IIILKQKEMRNVTNILIVNLSFSDLLVAIMCLPFTFVYTLMDHWVFGEAMCKLNPFVQCV 122

Qy        138 SVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLM------- 190
              |: |: :||  |::::   | :|     : | |     :||:::   :||:|:
Db        123 SITVSIFSLVLIAVERHQLIINPRGWRPNNRHAYVGIAVIWVLAVASSLPFLIYQVMTDE 182

Qy        191 SFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYCYFKI 250
              |::|    |           : | :  : |:: |  | | :::||:  |:  |  |||||
Db        183 PFQNVTLDAYKDK-------YVCFD-QFPSDSHRLSYTTLLLVLQYFGPLCFIFICYFKI 234

Qy        251 LQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKD 310
              :: :    :|    :     | ||  |   |::| :|:::|| |  ||||||: | | |
Db        235 YIRLKR----RNNMMDKMRDNKYRSSET---KRINIMLLSIVVAFAVCWLPLTIFNTVFD 287

Qy        311 FKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKR 353
              :  :          : :  |: ||     ||: : :| :  :|
Db        288 WNHQIIATCNHNLLFLL-CHLTAMISTCVNPIFYGFLNKNFQR 329


RESULT 4
US-10-987-856-16
; Sequence 16, Application US/10987856
; Publication No. US20060014242A1
; GENERAL INFORMATION:
;  APPLICANT: GERALD, CHRISTOPHE P.G.
;  APPLICANT:  WEINSHANK, RICHARD L
;  APPLICANT:  WALKER, MARY W
;  APPLICANT:  BRANCHEK, THERESA
;  TITLE OF INVENTION: MODIFYING FEEDING BEHAVIOR, COMPOUNDS USEFUL IN SUCH METHODS, AN
;  TITLE OF INVENTION:  ENCODING A HYPOTHALAMIC ATYPICAL NEUROPEPTIDE Y/PEPTIDE YY RECE
;  FILE REFERENCE: 1795/46166BZA
;  CURRENT APPLICATION NUMBER: US/10/987,856
;  CURRENT FILING DATE:  2004-11-12
;  PRIOR APPLICATION NUMBER: US/09/962,646
;  PRIOR FILING DATE: 2001-09-24
;  PRIOR APPLICATION NUMBER: 09/200,673
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;  PRIOR FILING DATE: 1998-11-25
;  PRIOR APPLICATION NUMBER: 08/566,096
;  PRIOR FILING DATE: 1995-12-01
;  PRIOR APPLICATION NUMBER: 08/349,025
;  PRIOR FILING DATE: 1994-12-01
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 381
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-987-856-16

  Query Match            15.6%;  Score 324;  DB 9;  Length 381;
  Best Local Similarity  25.5%;  Pred. No. 2.3e-21;
  Matches   91;  Conservative   67;  Mismatches  139;  Indels   60;  Gaps    9;

Qy         37 AEAIAAQGIDDITVDFY-------------------------IRSIFTFLYGFLFVLGI 70
              |||    | :::: |: |                         :: :    |  : :||:
Db          6 AEADENQTVEEMKVEQYGPQTTPRGELVPDPEPELIDSTKLIEVQVVLILAYCSIILLGV 65

Qy         71 FGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHL 130
               ||  |: | : | :::  | |: ||   ||::    :| |  | :  :|  | |:|||
Db         66 IGNSLVIHVVIKFKSMRTVTNFFIANLAVADLLVNTLCLPFTLTYTLMGEWKMGPVLCHL 125

Qy        131 VPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLM 190
              || :   :| |:: :|| |:||:   |    :  :| | :  |  | | :| |:  |  :
Db        126 VPYAQGLAVQVSTITLTVIALDRHRCIVYHLESKISKRISFLIIGLAWGISALLASPLAI 185

Qy        191 SFEH----VDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGT----TVMLLQFVVPMAV 242
                |:    :   | :           | |  |  |  : ||||    : :|: :|:|: :
Db        186 FREYSLIEIIPDFEIVA---------CTE-KWPGE-EKSIYGTVYSLSSLLILYVLPLGI 234

Qy        243 ITYCYFKILQKVSKDMI--IQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 300
              |:: | :|  |:   :    |  : |           |::|   :|: :|| |   ||
Db        235 ISFSYTRIWSKLKNHVSPGAANDHYHQ-----------RRQKTTKMLVCVVVVFAVSWL 282

Qy        301 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLS 357
              ||    |  |   :  ||    : :  |:|||    ||||: |:    ::: ||
Db        283 PLHAFQLAVDIDSQVLDLKEYKLIFTV-FHIIAMCSTFANPLLYGWMNSNYRKAFLS 338


RESULT 5
US-10-987-856-17
; Sequence 17, Application US/10987856
; Publication No. US20060014242A1
; GENERAL INFORMATION:
;  APPLICANT: GERALD, CHRISTOPHE P.G.
;  APPLICANT:  WEINSHANK, RICHARD L
;  APPLICANT:  WALKER, MARY W
;  APPLICANT:  BRANCHEK, THERESA
;  TITLE OF INVENTION: MODIFYING FEEDING BEHAVIOR, COMPOUNDS USEFUL IN SUCH METHODS, AND
;  TITLE OF INVENTION:  ENCODING A HYPOTHALAMIC ATYPICAL NEUROPEPTIDE Y/PEPTIDE YY RECEP
;  FILE REFERENCE: 1795/46166BZA
;  CURRENT APPLICATION NUMBER: US/10/987,856
;  CURRENT FILING DATE:  2004-11-12
;  PRIOR APPLICATION NUMBER: US/09/962,646
;  PRIOR FILING DATE: 2001-09-24
;  PRIOR APPLICATION NUMBER: 09/200,673
;  PRIOR FILING DATE: 1998-11-25
;  PRIOR APPLICATION NUMBER: 08/566,096
;  PRIOR FILING DATE: 1995-12-01
;  PRIOR APPLICATION NUMBER: 08/349,025
;  PRIOR FILING DATE: 1994-12-01
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
;   LENGTH: 375
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-987-856-17

  Query Match            15.1%;  Score 314;  DB 9;  Length 375;
  Best Local Similarity  26.1%;  Pred. No. 1.8e-20;
  Matches   88;  Conservative   72;  Mismatches  155;  Indels   22;  Gaps    8;

Qy         62 YGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDW 121
              |    |:|: ||  ::    | |   :  |: : || |:| ::      |:|  | :   |
Db         48 YSIETVVGVLGNLCLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYW 107

Qy        122 AFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIVS 181
               ||  :| :         || |:  ||  ::|::   | :||    || ||      |||:::
Db        108 IFGETLCKMSAFIQCMSVTVSILSLVLVALERHQLIINPTGWKPSISQAYLGIVLIWVIA 167

Qy        182 TLINLPYLMS--FEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVP 239
              :::||:| :   |:|    : :  |       | | :|   : | || | ::| |: :|
Db        168 CVLSLPPLANSILENVFHKNHSKALEFLADKVVCTE-SWPLAHHRTIYTTFLLLFQYCLP 226

Qy        240 MAVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCW 299
              :  |  || :| ::: :    |   | :  |    |:       |:|| :|: ||| |   |
Db        227 LGFILVCYARIYRRLQR----QGRVFHKG-TYSLRA---GHMKQVNVVLVVMVVAFAVLW 278

Qy        300 LPLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKI 359
              ||| : | ::|:  |   :      : :  |::||:    || :: :|    |:   : :
Db        279 LPLHVFNSLEDWHHEAIPICHGNLIFLV-CHLLAMASTCVNPFIYGFLNTNFKKEIKALV 337

Qy        360 LNSTEGSKKAGGSGLRGIQLHDLLPTST-HSDRCAGN 395
              |   : :           ::  : || || |::   |:
Db        338 LTCQQSAP---------LEESEHLPLSTVHTEVSKGS 365


RESULT 6
US-10-992-577-6
; Sequence 6, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
;  APPLICANT: Gerald, Christophe P.G.
;  APPLICANT:  Jones, Kenneth A.
;  APPLICANT:  Bonini, James A.
;  APPLICANT:  Borowsky, Beth E.
;  APPLICANT:  Craig, Douglas A.
;  TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
;  TITLE OF INVENTION:  And Uses Thereof
;  FILE REFERENCE: 57155-D/JPW
;  CURRENT APPLICATION NUMBER: US/10/992,577
;  CURRENT FILING DATE:  2004-11-18
;  PRIOR APPLICATION NUMBER: US/09/538,036
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: 09/405,558
;  PRIOR FILING DATE: 1999-09-24
;  PRIOR APPLICATION NUMBER: 09/255,368
;  PRIOR FILING DATE: 1999-02-22
;  PRIOR APPLICATION NUMBER: 09/161,113
;  PRIOR FILING DATE: 1998-09-25
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 420
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-992-577-6

  Query Match            14.7%;  Score 304;  DB 9;  Length 420;
  Best Local Similarity  25.7%;  Pred. No. 1.6e-19;
  Matches   81;  Conservative   73;  Mismatches  143;  Indels   18;  Gaps    6;

Qy         50 VDFY-----IRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLIL 104
              |::|     : :||    |  :| | : ||  | : | ||| : :  |:|:|||  :||::
Db         35 VNYYLHQPQVAAIFIISYFLIFFLCMMGNTVVCFIVMRNKHMHTVTNLFILNLAISDLLV 94

Qy        105 VFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQP 164
                :|:|    :   | ||: || :  |     ||  : ::| ||::|:|  :  | |
Db         95 GIFCMPITLLDNIIAGWPFGNTMCKISGLVQGISVAASVFTLVAIAVDRFQCVVYPFKPK 154

Qy        165 VSIRQALAITFLIWIVSTLINLPYLMSFEHVDGSFY-----VQPGETPYCGHFCDEANWQ 219
              ::|: |  |  :||:::  |  |  :     :  :|      |   :|   ::| | :|
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Db        155 LTIKTAFVIIMIIWVLAITIMSPSAVMLHVQEEKYYRVRLNSQNKTSPV--YWCRE-DWP 211

Qy        220 SENSRKIYGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATS 279

Db        212 NQEMRKIYTTVLFANIYLAPLSLIVIMYGRIGISLFRAAVPHTGR----KNQEQWHVVSR 267

Qy        280 RKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKK-EPEWLKRQPFFWAINAHVIAMSLVV 338

Db        268 KKQKIIKMLLIVALLFILSWLPLWTLMMLSDYADLSPNELQIINIYIYPFAHWLAFGNSS 327

Qy        339 WNPLLFFWLTRKQKR 353

Db        328 VNPIIYGFFNENFRR 342


RESULT 7
US-10-510-018-2
; Sequence 2, Application US/10510018
; Publication No. US20050244896A1
; GENERAL INFORMATION:
;  APPLICANT: Golz, Stefan
;  APPLICANT:  Bruggemeier, Ulf
;  APPLICANT:  Weingarten, Bernhard
;  TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
;  TITLE OF INVENTION:  Neuropeptide FF Receptor 2 (NPFF2)
;  FILE REFERENCE: Le A 35 945
;  CURRENT APPLICATION NUMBER: US/10/510,018
;  CURRENT FILING DATE:  2004-10-01
;  PRIOR APPLICATION NUMBER: PCT/EP2003/002962
;  PRIOR FILING DATE: 2003-03-21
;  PRIOR APPLICATION NUMBER: EP 02007270.8
;  PRIOR FILING DATE: 2002-04-02
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
;   LENGTH: 522
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-510-018-2

  Query Match             14.7%;  Score 304;  DB 9;  Length 522;
  Best Local Similarity   25.7%;  Pred. No. 2.1e-19;
  Matches   81;  Conservative   73;  Mismatches  143;  Indels   18;  Gaps    6;

Qy         50 VDFY-----IRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLIL 104

Db        137 VNYYLHQPQVAAIFIISYFLIFFLCMMGNTVVCFIVMRNKHMHTVTNLFILNLAISDLLV 196

Qy        105 VFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQP 164

Db        197 GIFCMPITLLDNIIAGWPFGNTMCKISGLVQGISVAASVFTLVAIAVDRFQCVVYPFKPK 256

Qy        165 VSIRQALAITFLIWIVSTLINLPYLMSFEHVDGSFY-----VQPGETPYCGHFCDEANWQ 219

Db        257 LTIKTAFVIIMIIWVLAITIMSPSAVMLHVQEEKYYRVRLNSQNKTSPV--YWCRE-DWP 313

Qy        220 SENSRKIYGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATS 279

Db        314 NQEMRKIYTTVLFANIYLAPLSLIVIMYGRIGISLFRAAVPHTGR----KNQEQWHVVSR 369

Qy        280 RKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKK-EPEWLKRQPFFWAINAHVIAMSLVV 338

Db        370 KKQKIIKMLLIVALLFILSWLPLWTLMMLSDYADLSPNELQIINIYIYPFAHWLAFGNSS 429

Qy        339 WNPLLFFWLTRKQKR 353

Db        430 VNPIIYGFFNENFRR 444


RESULT 8
US-10-055-877-248
; Sequence 248, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
;  APPLICANT: DeCristofaro, Marc
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Miller, Charles
;  APPLICANT:  Tchernev, Velizar
;  APPLICANT:  Zhong, Mei
;  APPLICANT:  Anderson, David
;  APPLICANT:  Ballinger, Robert
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Spytek, Kimberly
;  APPLICANT:  Ratelli, Luca
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Guo, Xiaojia
;  APPLICANT:  Zerhusen, Bryan
;  APPLICANT:  Andrew, David
;  APPLICANT:  Mezes, Peter
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Burgess, Cahterine
;  APPLICANT:  Eisen, Andrew
;  APPLICANT:  Wolenc, Adam
;  APPLICANT:  Baumgartner, Jason
;  APPLICANT:  Shimkets, Richard
;  APPLICANT:  Gusev, Vladimir
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Taupier Jr., Raymond
;  APPLICANT:  Pena, Carol
;  APPLICANT:  Shenoy, Suresh
;  APPLICANT:  Li, Li
;  APPLICANT:  Casman, Stacie
;  APPLICANT:  Boldog, Ference
;  TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
;  FILE REFERENCE: 21402-251
;  CURRENT APPLICATION NUMBER: US/10/055,877
;  CURRENT FILING DATE:  2002-01-22
;  PRIOR APPLICATION NUMBER: 60/262,892
;  PRIOR FILING DATE: 2001-01-19
;  PRIOR APPLICATION NUMBER: 60/263,598
;  PRIOR FILING DATE: 2001-01-23
;  PRIOR APPLICATION NUMBER: 60/263,799
;  PRIOR FILING DATE: 2001-01-24
;  PRIOR APPLICATION NUMBER: 60/264,117
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: 60/264,139
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: 60/264,478
;  PRIOR FILING DATE: 2001-01-26
;  PRIOR APPLICATION NUMBER: 60/263,351
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: 60/272,870
;  PRIOR FILING DATE: 2001-03-02
;  PRIOR APPLICATION NUMBER: 60/275,990
;  PRIOR FILING DATE: 2001-03-14
;  PRIOR APPLICATION NUMBER: 60/275,927
;  PRIOR FILING DATE: 2001-03-14
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 512
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 248
;   LENGTH: 254
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: 7tm_1, 7
;   OTHER INFORMATION: transmembrane receptor domain
US-10-055-877-248

  Query Match             13.8%;  Score 286.5;  DB 9;  Length 254;
  Best Local Similarity   26.9%;  Pred. No. 3.3e-18;
  Matches   76;  Conservative   62;  Mismatches  106;  Indels   39;  Gaps    7;

Qy         72 GNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLV 131

Db          1 GNLLVILVILRTKKLRTPTNIFLLNLAVADLLFLLTLPPWALYYLVGGDWVFGDALCKLV 60
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```
Qy        132 PLSNSCSVFVTSWSLTAISLDKFLHINDPT--KQPVSIRQALAITFLIWIVSTLINLPYL 189
Db         61 GALFVVNGYASILLLTAISIDRYLAIVHPLRYRRIRTPRRAKVLILLVWVLALLLSLPPL 120

Qy        190 MSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYCYFK 249
Db        121 L-FSWLR---TVEEGNTTVC-----LIDFPEESVKRSYVLLSTLVGFVLPLLVILVCYTR 171

Qy        250 ILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVK 309
Db        172 ILRTLRK----------RARSQRSLKRRSSSERKAAKMLLVVVVVFVLCWLPYHIVLLLD 221

Qy        310 DFKKEPEWLKRQPFFWAINAHVIAMSLVVW--------NPLLF 344
Db        222 SLCLLSIW----------RVLPTALLITLWLAYVNSCLNPIIY 254
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RESULT 9
US-10-055-877-327
; Sequence 327, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Cahterine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shimkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ference
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 327
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 7tm_1, 7
; OTHER INFORMATION: transmembrane receptor domain consensus sequence
US-10-055-877-327

Query Match 13.8%; Score 286.5; DB 9; Length 254;
Best Local Similarity 26.9%; Pred. No. 3.3e-18;
Matches 76; Conservative 62; Mismatches 106; Indels 39; Gaps 7;

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Qy         72 GNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLV 131
Db          1 GNLLVILVILRTKKLRTPTNIFLLNLAVADLLFLLTLPPWALYYLVGGDWVFGDALCKLV 60

Qy        132 PLSNSCSVFVTSWSLTAISLDKFLHINDPT--KQPVSIRQALAITFLIWIVSTLINLPYL 189
Db         61 GALFVVNGYASILLLTAISIDRYLAIVHPLRYRRIRTPRRAKVLILLVWVLALLLSLPPL 120

Qy        190 MSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYCYFK 249
Db        121 L-FSWLR---TVEEGNTTVC-----LIDFPEESVKRSYVLLSTLVGFVLPLLVILVCYTR 171

Qy        250 ILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVK 309
Db        172 ILRTLRK----------RARSQRSLKRRSSSERKAAKMLLVVVVVFVLCWLPYHIVLLLD 221

Qy        310 DFKKEPEWLKRQPFFWAINAHVIAMSLVVW--------NPLLF 344
Db        222 SLCLLSIW----------RVLPTALLITLWLAYVNSCLNPIIY 254
```

RESULT 10
US-10-055-877-340
; Sequence 340, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Cahterine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shimkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie

```
;  APPLICANT:  Boldog, Ference
;  TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
;  FILE REFERENCE: 21402-251
;  CURRENT APPLICATION NUMBER: US/10/055,877
;  CURRENT FILING DATE:  2002-01-22
;  PRIOR APPLICATION NUMBER: 60/262,892
;  PRIOR FILING DATE: 2001-01-19
;  PRIOR APPLICATION NUMBER: 60/263,598
;  PRIOR FILING DATE: 2001-01-23
;  PRIOR APPLICATION NUMBER: 60/263,799
;  PRIOR FILING DATE: 2001-01-24
;  PRIOR APPLICATION NUMBER: 60/264,117
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: 60/264,139
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: 60/264,478
;  PRIOR FILING DATE: 2001-01-26
;  PRIOR APPLICATION NUMBER: 60/263,351
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: 60/272,870
;  PRIOR FILING DATE: 2001-03-02
;  PRIOR APPLICATION NUMBER: 60/275,990
;  PRIOR FILING DATE: 2001-03-14
;  PRIOR APPLICATION NUMBER: 60/275,927
;  PRIOR FILING DATE: 2001-03-14
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 512
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 340
;   LENGTH: 254
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: 7tm_1, 7
;   OTHER INFORMATION: transmembrane receptor domain consensus sequence
US-10-055-877-340

  Query Match             13.8%;  Score 286.5;  DB 9;  Length 254;
  Best Local Similarity   26.9%;  Pred. No. 3.3e-18;
  Matches   76;  Conservative   62;  Mismatches  106;  Indels   39;  Gaps    7;

Qy          72 GNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLV 131
               ||  |:  : | |:|::  |:|||||    ||: : |  |   :| :  || ||  :| ||
Db           1 GNLLVILVILRTKKLRTPTNIFLLNLAVADLLFLLTLPPWALYYLVGGDWVFGDALCKLV 60

Qy         132 PLSNSCSVFVTSWSLTAISLDKFLHINDPT--KQPVSIRQALAITFLIWIVSTLINLPYL 189
                 : : :   |||||:|::| |  |    ::  : |:|  :  |:|::: |::|| |
Db          61 GALFVVNGYASILLLTAISIDRYLAIVHPLRYRRIRTPRRAKVLILLVWVLALLLSLPPL 120

Qy         190 MSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYCYFK 249
               : |  :     |: | |  |       ::  |: :: |     |: ||:|: ||  || :
Db         121 L-FSWLR---TVEEGNTTVC-----LIDFPEESVKRSYVLLSTLVGFVLPLLVILVCYTR 171

Qy         250 ILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVK 309
               ||: : |          :: :|:     :| ::|   :|: :|| |: |||| :: |:
Db         172 ILRTLRK----------RARSQRSLKRRSSSERKAAKMLLVVVVVFVLCWLPYHIVLLLD 221

Qy         310 DFKKEPEWLKRQPFFWAINAHVIAMSLVVW--------NPLLF 344
                        |             |: : :|         ||:::
Db         222 SLCLLSIW----------RVLPTALLITLWLAYVNSCLNPIIY 254


RESULT 11
US-10-877-346-83
; Sequence 83, Application US/10877346
; Publication No. US20060014153A1
; GENERAL INFORMATION:
;  APPLICANT: Gerlach, Valerie L
;  APPLICANT:  MacDougall, John R
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Stone, David
;  APPLICANT:  Gunther, Erik
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Grosse, William M
;  APPLICANT:  Alsobrook II, John P
;  APPLICANT:  Lepley, Denise M
;  APPLICANT:  Burgess, Catherine E
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Leach, Martin D
;  APPLICANT:  Shimkets, Richard A
;  TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-124
;  CURRENT APPLICATION NUMBER: US/10/877,346
;  CURRENT FILING DATE:  2004-06-25
;  PRIOR APPLICATION NUMBER: US/09/964,956
;  PRIOR FILING DATE: 2001-09-26
;  PRIOR APPLICATION NUMBER: 60/235,631
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: 60/235,633
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: 60/235,808
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: 60/236,064
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: 60/236,065
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: 60/236,066
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: 60/236,135
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: 60/237,434
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/238,321
;  PRIOR FILING DATE: 2000-10-05
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 127
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
;   LENGTH: 254
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: 7
;   OTHER INFORMATION: transmembrane receptor Consensus Sequence
US-10-877-346-83

  Query Match             13.8%;  Score 286.5;  DB 9;  Length 254;
  Best Local Similarity   26.9%;  Pred. No. 3.3e-18;
  Matches   76;  Conservative   62;  Mismatches  106;  Indels   39;  Gaps    7;

Qy          72 GNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLV 131
               ||  |:  : | |:|::  |:|||||    ||: : |  |   :| :  || ||  :| ||
Db           1 GNLLVILVILRTKKLRTPTNIFLLNLAVADLLFLLTLPPWALYYLVGGDWVFGDALCKLV 60

Qy         132 PLSNSCSVFVTSWSLTAISLDKFLHINDPT--KQPVSIRQALAITFLIWIVSTLINLPYL 189
                 : : :   |||||:|::| |  |    ::  : |:|  :  |:|::: |::|| |
Db          61 GALFVVNGYASILLLTAISIDRYLAIVHPLRYRRIRTPRRAKVLILLVWVLALLLSLPPL 120

Qy         190 MSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYCYFK 249
               : |  :     |: | |  |       ::  |: :: |     |: ||:|: ||  || :
Db         121 L-FSWLR---TVEEGNTTVC-----LIDFPEESVKRSYVLLSTLVGFVLPLLVILVCYTR 171

Qy         250 ILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVK 309
               ||: : |          :: :|:     :| ::|   :|: :|| |: |||| :: |:
Db         172 ILRTLRK----------RARSQRSLKRRSSSERKAAKMLLVVVVVFVLCWLPYHIVLLLD 221

Qy         310 DFKKEPEWLKRQPFFWAINAHVIAMSLVVW--------NPLLF 344
                        |             |: : :|         ||:::
Db         222 SLCLLSIW----------RVLPTALLITLWLAYVNSCLNPIIY 254


RESULT 12
US-10-992-577-8
```

; Sequence 8, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; TITLE OF INVENTION: And Uses Thereof
; FILE REFERENCE: 57155-D/JPW
; CURRENT APPLICATION NUMBER: US/10/992,577
; CURRENT FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: US/09/538,036
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/405,558
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 09/255,368
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-992-577-8

Query Match 13.8%; Score 285.5; DB 9; Length 430;
Best Local Similarity 24.6%; Pred. No. 7.5e-18;
Matches 96; Conservative 81; Mismatches 161; Indels 53; Gaps 12;

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Qy         17 PSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFY------IRSIFTFLYGFLFVLGI 70
              ||   |      | ||:  :   |       ::|   |      : ::|   | :|:| :
Db          5 PSQPPNSSWPLSQNGTNTEATPA------TNLTFSSYYQHTSPVAAMFIVAYALIFLLCM 58

Qy         71 FGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHL 130
               ||  | : | :|: : :  |:|:|||  :||::    :| |    :   | | :  | :
Db         59 VGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDNATCKM 118

Qy        131 VPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLM 190
              |    ||  : ::| ||:::|  |   | :: :::|:||    :|| :: ||  |  :
Db        119 SGLVQGMSVSASVFTLVAIAVERFRCIVHPFREKLTLRKALVTIAVIWALALLIMCPSAV 178

Qy        191 SF-----EHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITY 245
              :      ||    | |      |  : | || |  :  |::| | :    :: |:|:|
Db        179 TLTVTREEH---HFMVDARNRSYPLYSCWEA-WPEKGMRRVYTTVLFSHIYLAPLALIVV 234

Qy        246 CYFKILQKVSKDMIIQNAQFCQSLTQ----KQRSD--ATSRKKKVNYILIAMVVTFIGCW 299
              | :| :|:           ||:      :: :|  |: |: :| ::|: : : |   |
Db        235 MYARIARKL----------CQAPGPAPGGEEAADPRASRRRARVVHMLVMVALFFTLSW 283

Qy        300 LPLTLLNLVKDFKK--EPE----WLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKR 353
              |||  | |: |: :   |:     :   ||     || :|     ||::: :    :|
Db        284 LPLWALLLLIDYGQLSAPQLHLVTVYAFPF-----AHWLAFFNSSANPIIYGYFNENFRR 338

Qy        354 ----SGLSKILNSTEGSKKAGGSGLRGIQLH 380
                  :  :::     || |   |   | ||
Db        339 GFQAAFRARLCPRPSGSHKEAYSERPGGLLH 369
```

RESULT 13
US-10-508-892-2
; Sequence 2, Application US/10508892
; Publication No. US20060014218A1
; GENERAL INFORMATION:
; APPLICANT: Golz, Stefan
; APPLICANT: Bruggemeier, Ulf
; APPLICANT: Weingartner, Bernhard
; TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
; TITLE OF INVENTION: Neuropeptide FF Receptor 1 (NPFF1)
; FILE REFERENCE: Le A 35 944
; CURRENT APPLICATION NUMBER: US/10/508,892
; CURRENT FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: PCT/EP03/02685
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: EP 02006654.4
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-508-892-2

Query Match 13.8%; Score 285.5; DB 9; Length 430;
Best Local Similarity 24.6%; Pred. No. 7.5e-18;
Matches 96; Conservative 81; Mismatches 161; Indels 53; Gaps 12;

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Qy         17 PSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFY------IRSIFTFLYGFLFVLGI 70
              ||   |      | ||:  :   |       ::|   |      : ::|   | :|:| :
Db          5 PSQPPNSSWPLSQNGTNTEATPA------TNLTFSSYYQHTSPVAAMFIVAYALIFLLCM 58

Qy         71 FGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHL 130
               ||  | : | :|: : :  |:|:|||  :||::    :| |    :   | | :  | :
Db         59 VGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDNATCKM 118

Qy        131 VPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLM 190
              |    ||  : ::| ||:::|  |   | :: :::|:||    :|| :: ||  |  :
Db        119 SGLVQGMSVSASVFTLVAIAVERFRCIVHPFREKLTLRKALVTIAVIWALALLIMCPSAV 178

Qy        191 SF-----EHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITY 245
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Db        179 TLTVTREEH---HFMVDARNRSYPLYSCWEA-WPEKGMRRVYTTVLFSHIYLAPLALIVV 234

Qy        246 CYFKILQKVSKDMIIQNAQFCQSLTQ----KQRSD--ATSRKKKVNYILIAMVVTFIGCW 299
              | :| :|:           ||:      :: :|  |: |: :| ::|: : : |   |
Db        235 MYARIARKL----------CQAPGPAPGGEEAADPRASRRRARVVHMLVMVALFFTLSW 283

Qy        300 LPLTLLNLVKDFKK--EPE----WLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKR 353
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Db        284 LPLWALLLLIDYGQLSAPQLHLVTVYAFPF-----AHWLAFFNSSANPIIYGYFNENFRR 338

Qy        354 ----SGLSKILNSTEGSKKAGGSGLRGIQLH 380
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Db        339 GFQAAFRARLCPRPSGSHKEAYSERPGGLLH 369
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RESULT 14
US-11-223-294-54
; Sequence 54, Application US/11223294
; Publication No. US20060035332A1
; GENERAL INFORMATION:
; APPLICANT: HINUMA, Shuji
; APPLICANT: YOSHIDA, Hiromi
; APPLICANT: HABATA, Yugo
; APPLICANT: HOSOYA, Masaki
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: Novel RFRP-3 And Its DNA
; FILE REFERENCE: 2944US0P
; CURRENT APPLICATION NUMBER: US/11/223,294
; CURRENT FILING DATE: 2005-09-09
; PRIOR APPLICATION NUMBER: US/10/487,634
; PRIOR FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: PCT/JP02/08466
; PRIOR FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: JP 2001-254826
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 54
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Human
US-11-223-294-54

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  Query Match             13.8%;  Score 285.5;  DB 11;  Length 430;
  Best Local Similarity   24.6%;  Pred. No. 7.5e-18;
  Matches   96;  Conservative   81;  Mismatches  161;  Indels   53;  Gaps   12;

Qy         17 PSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFY------IRSIFTFLYGFLFVLGI 70
              ||   |      | ||:  :   |       ::|   |       : ::|   | :|:| :
Db          5 PSQPPNSSWPLSQNGTNTEATPA------TNLTFSSYYQHTSPVAAMFIVAYALIFLLCM 58

Qy         71 FGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHL 130
              ||   | : | :|: : :  |:|:|||  :||::    :|  |    :   | | :  | :
Db         59 VGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDNATCKM 118

Qy        131 VPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLM 190
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Db        119 SGLVQGMSVSASVFTLVAIAVERFRCIVHPFREKLTLRKALVTIAVIWALALLIMCPSAV 178

Qy        191 SF-----EHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITY 245
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Db        179 TLTVTREEH---HFMVDARNRSYPLYSCWEA-WPEKGMRRVYTTVLFSHIYLAPLALIVV 234

Qy        246 CYFKILQKVSKDMIIQNAQFCQSLTQ----KQRSD--ATSRKKKVNYILIAMVVTFIGCW 299
              | :| :|:           ||:      :: :|  |: |: :| ::|: : :  |   |
Db        235 MYARIARKL-----------CQAPGPAPGGEEAADPRASRRRARVVHMLVMVALFFTLSW 283

Qy        300 LPLTLLNLVKDFKK--EPE----WLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKR 353
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Db        284 LPLWALLLLIDYGQLSAPQLHLVTVYAPPF-----AHWLAFFNSSANPIIYGYFNENFRR 338

Qy        354 ----SGLSKILNSTEGSKKAGGSGLRGIQLH 380
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Db        339 GFQAAFRARLCPRPSGSHKEAYSERPGGLLH 369


RESULT 15
US-10-992-577-2
; Sequence 2, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
;  APPLICANT: Gerald, Christophe P.G.
;  APPLICANT:  Jones, Kenneth A.
;  APPLICANT:  Bonini, James A.
;  APPLICANT:  Borowsky, Beth E.
;  APPLICANT:  Craig, Douglas A.
;  TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
;  TITLE OF INVENTION:  And Uses Thereof
;  FILE REFERENCE: 57155-D/JPW
;  CURRENT APPLICATION NUMBER: US/10/992,577
;  CURRENT FILING DATE:  2004-11-18
;  PRIOR APPLICATION NUMBER: US/09/538,036
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: 09/405,558
;  PRIOR FILING DATE: 1999-09-24
;  PRIOR APPLICATION NUMBER: 09/255,368
;  PRIOR FILING DATE: 1999-02-22
;  PRIOR APPLICATION NUMBER: 09/161,113
;  PRIOR FILING DATE: 1998-09-25
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 432
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-10-992-577-2

  Query Match             13.8%;  Score 285.5;  DB 9;  Length 432;
  Best Local Similarity   24.3%;  Pred. No. 7.5e-18;
  Matches   89;  Conservative   78;  Mismatches  139;  Indels   61;  Gaps   11;

Qy         17 PSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFY------IRSIFTFLYGFLFVLGI 70
              ||   |      ||| :: : | :      :|   |       : ::|   |  :|:| :
Db          5 PSQPPNGSWPLGQNGSDVETSMATS------LTFSSYYQHSSPVAAMFIAAYVLIFLLCM 58

Qy         71 FGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHL 130
              ||   | : | :|: ::: |:|:|||  :||::    :|  |    :   | | :  | :
Db         59 VGNTLVCFIVLKNRHMRTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDNATCKM 118

Qy        131 VPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLM 190
              |    ||  : ::| ||::::|  |  | :: :::|:||    :|| :: ||  |  :
Db        119 SGLVQGMSVSASVFTLVAIAVERFRCIVHPFREKLTLRKALFTIAVIWALALLIMCPSAV 178

Qy        191 SF-----EHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITY 245
             :      ||    | :      | : | || |  :  ||:|   :    ::||:|:|
Db        179 TLTVTREEH---HFMLDARNRSYPLYSCWEA-WPEKGMRKVYTAVLFAHIYLVPLALIVV 234

Qy        246 CYFKILQKVSKDMIIQNAQFCQSLTQKQRSD-------ATSRKK-KVNYILIAMVVTFIG 297
              | :| :|:           ||:    : ::        |||:: :| ::|: : : |
Db        235 MYVRIARKL-----------CQAPGPARDTEEAVAEGGRTSRRRARVVHMLVMVALFFTL 283

Qy        298 CWLPLTLLNLVKDFKKEPEWLKRQPFFWAINAH---VIAMSLVVW--------NPLLFFW 346
              |||| :| |: |: :  |          :  |   | |   |  |         ||::: :
Db        284 SWLPLWVLLLLIDYGELSE----------LQLHLLSVYAFPLAHWLAFFHSSANPIIYGY 333

Qy        347 LTRKQKR 353
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Db        334 FNENFRR 340


Search completed: May  8, 2006, 09:38:33
Job time : 29 secs
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GenCore version 5.1.8

OM protein - protein search, using sw model

Run on: May 8, 2006, 09:33:48 ; Search time 47 Seconds
(without alignments)
698.346 Million cell updates/sec

Title: US-10-650-467-105
Perfect score: 2074
Sequence: 1 MVSSAATISTISTTTTPSTI.....QLHDLLPTSTHSDRCAGNSF 397

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2074	100.0	397	2	US-09-721-870-105	Sequence 105, App
2	2074	100.0	499	2	US-09-721-870-40	Sequence 40, Appl
3	1899	91.6	433	2	US-09-721-870-107	Sequence 107, App
4	607.5	29.3	450	2	US-09-721-870-16	Sequence 16, Appl
5	529	25.5	600	2	US-09-693-746-2	Sequence 2, Appli
6	515.5	24.9	376	2	US-09-721-870-22	Sequence 22, Appl
7	485.5	23.4	457	2	US-09-721-870-26	Sequence 26, Appl
8	461.5	22.3	365	2	US-09-721-870-36	Sequence 36, Appl
9	460.5	22.2	387	2	US-09-721-870-14	Sequence 14, Appl
10	458	22.1	381	2	US-09-721-870-12	Sequence 12, Appl
11	458	22.1	402	2	US-09-721-870-8	Sequence 8, Appli
12	458	22.1	404	2	US-09-721-870-6	Sequence 6, Appli
13	458	22.1	406	2	US-09-721-870-10	Sequence 10, Appl
14	388	18.7	458	2	US-09-693-746-6	Sequence 6, Appli
15	386	18.6	370	2	US-08-513-974B-26	Sequence 26, Appl
16	386	18.6	370	2	US-08-513-974B-323	Sequence 323, App
17	386	18.6	370	2	US-09-172-353-5	Sequence 5, Appli
18	386	18.6	370	2	US-08-776-971-21	Sequence 21, Appl
19	386	18.6	370	2	US-08-776-971-104	Sequence 104, App
20	386	18.6	370	2	US-09-799-955-5	Sequence 5, Appli
21	386	18.6	370	2	US-09-461-436B-26	Sequence 26, Appl
22	386	18.6	370	2	US-09-576-290-21	Sequence 21, Appl
23	386	18.6	370	2	US-09-576-290-104	Sequence 104, App
24	386	18.6	370	2	US-09-716-147-21	Sequence 21, Appl
25	386	18.6	370	2	US-09-716-147-104	Sequence 104, App
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27	385.5	18.6	370	2	US-09-172-353-3	Sequence 3, Appli
28	385.5	18.6	370	2	US-09-799-955-2	Sequence 2, Appli
29	385.5	18.6	370	2	US-09-799-955-3	Sequence 3, Appli
30	382	18.4	376	2	US-09-721-870-44	Sequence 44, Appl
31	373.5	18.0	370	2	US-09-172-353-7	Sequence 7, Appli
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33	371.5	17.9	369	2	US-09-170-496D-178	Sequence 178, App
34	368.5	17.8	369	2	US-09-172-353-6	Sequence 6, Appli
35	368.5	17.8	369	2	US-09-799-955-6	Sequence 6, Appli
36	368.5	17.8	369	2	US-09-170-496D-26	Sequence 26, Appl
37	368	17.7	434	2	US-09-721-870-117	Sequence 117, App
38	367.5	17.7	427	2	US-09-721-870-115	Sequence 115, App
39	361.5	17.4	370	2	US-08-776-971-140	Sequence 140, App
40	361.5	17.4	370	2	US-09-576-290-140	Sequence 140, App
41	361.5	17.4	370	2	US-09-716-147-140	Sequence 140, App
42	356.5	17.2	371	1	US-08-415-818-6	Sequence 6, Appli
43	356.5	17.2	371	1	US-08-894-236-6	Sequence 6, Appli
44	356.5	17.2	371	1	US-08-919-624-4	Sequence 4, Appli
45	356.5	17.2	371	4	PCT-US96-01444-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-721-870-105
; Sequence 105, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Geary, Timothy G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/09/721,870
; CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-721-870-105

Query Match 100.0%; Score 2074; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 9e-165;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MVSSAATISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF 60

Qy         61 LYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKD 120
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Db         61 LYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKD 120

Qy        121 WAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 WAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIV 180

Qy        181 STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM 240
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Db        181 STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM 240

Qy        241 AVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 300

Qy        301 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLPFWLTRKQKRSGLSKIL 360
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Db        301 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLPFWLTRKQKRSGLSKIL 360

Qy        361 NSTEGSKKAGGSGLRGIQLHDLLPTSTHSDRCAGNSF 397
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Db        361 NSTEGSKKAGGSGLRGIQLHDLLPTSTHSDRCAGNSF 397


RESULT 2
US-09-721-870-40
; Sequence 40, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Geary, Timothy G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 28341/6223
;  CURRENT APPLICATION NUMBER: US/09/721,870
;  CURRENT FILING DATE:  2000-11-24
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
;   LENGTH: 499
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-721-870-40

  Query Match             100.0%;  Score 2074;  DB 2;  Length 499;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-164;
  Matches  397;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MVSSAATISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF 60
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Db        103 MVSSAATISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF 162

Qy         61 LYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKD 120
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Qy        121 WAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIV 180
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Db        223 WAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIV 282

Qy        181 STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM 240
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Db        283 STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM 342

Qy        241 AVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 300
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Db        343 AVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 402

Qy        301 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKIL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKIL 462

Qy        361 NSTEGSKKAGGSGLRGIQLHDLLPTSTHSDRCAGNSF 397
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Db        463 NSTEGSKKAGGSGLRGIQLHDLLPTSTHSDRCAGNSF 499


RESULT 3
US-09-721-870-107
; Sequence 107, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Geary, Timothy G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 28341/6223
;  CURRENT APPLICATION NUMBER: US/09/721,870
;  CURRENT FILING DATE:  2000-11-24
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
;   LENGTH: 433
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-721-870-107

  Query Match             91.6%;  Score 1899;  DB 2;  Length 433;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-150;
  Matches  364;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MVSSAATISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MVSSAATISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTF 60

Qy         61 LYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKD 120
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Qy        121 WAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 STLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPM 240
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Qy        241 AVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 300
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Db        241 AVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWL 300

Qy        301 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKIL 360
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Db        301 PLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKIL 360

Qy        361 NSTE 364
              ||||
Db        361 NSTE 364


RESULT 4
US-09-721-870-16
; Sequence 16, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Geary, Timothy G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 28341/6223
;  CURRENT APPLICATION NUMBER: US/09/721,870
;  CURRENT FILING DATE:  2000-11-24
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 450
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-721-870-16

  Query Match             29.3%;  Score 607.5;  DB 2;  Length 450;
  Best Local Similarity   35.3%;  Pred. No. 1.4e-42;
  Matches  119;  Conservative   76;  Mismatches  111;  Indels   31;  Gaps    7;

Qy         33 CIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNV 92
              || :   :  |  :| || | :|  :: ||  : ::|: ||| :: ::   |:| |  |:
Db          9 CIDVNAIL--QQFNDWTVLFEVRLGYSVLYFLILIIGLVGNGLLITSILMRKKL-SVANI 65

Qy         93 FLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLD 152
              ||:||  :||:|  ||:|:||  |  | | || :|| |||   : || ::|||| |::|
Db         66 FLINLAVSDLLLCITAVPITPVLAFMKRWIFGIIMCKLVPTCQAFSVLISSWSLCYIAID 125

Qy        153 KFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDGSFYVQPGET------ 206
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```
Db        126 RYRSIVTPLREPWSDRHARWLLMFTWVVAFLASYPL----------YYSQNLKTMVIENV 175

Qy        207 PYCGHFCDEANWQSENSRKI-YGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQF 265

Db        176 TLCGDFCGEFNWQSDEISKLTYTTSLLIIQLIIPAIIMSFCYLMILQKVQTDWLVDEGSM 235

Qy        266 CQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEW-------- 317

Db        236 ---LTAAQQAQTAVRKRRVMYVLILMVIVFMACWFPLSAVNLFRDLGMRFEFCQTVYKVL 292

Qy        318 LKRQPFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRS 354

Db        293 MMDQMYFKLLNVHVIAMTSIVWNPVLYFWMSKRHRRA 329


RESULT 5
US-09-693-746-2
; Sequence 2, Application US/09693746
; Patent No. 6835546
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Smith, Valdin G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
;  TITLE OF INVENTION:  Related To The Same
;  FILE REFERENCE: 6297.1cp
;  CURRENT APPLICATION NUMBER: US/09/693,746
;  CURRENT FILING DATE:  2000-10-20
;  PRIOR APPLICATION NUMBER: 09/425,676
;  PRIOR FILING DATE: 1999-10-22
;  NUMBER OF SEQ ID NOS: 168
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 600
;   TYPE: PRT
;   ORGANISM: D. melanogaster
US-09-693-746-2

  Query Match           25.5%;  Score 529;  DB 2;  Length 600;
  Best Local Similarity  30.5%;  Pred. No. 6.7e-36;
  Matches  136;  Conservative   76;  Mismatches  154;  Indels   80;  Gaps   12;

Qy          6 ATISTISTTTTPST---------ISNVITSHSNNGSCIQIAEAIAAQGID---DITVDFY 53

Db          2 ANLSWLSTITTTSSSISTSQLPLVSTTNWSLTSPGTTSAILADVAASDEDRSGGIIHNQF 61

Qy         54 IRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTP 113

Db         62 VQIFFYVLYATVFVLGVFGNVLVCYVVLRNRAMQTVTNIFITNLALSDILLCVLAVPFTP 121

Qy        114 WYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAI 173

Db        122 LYTFMGRWAFGRSLCHLVSFAQGCSIYISTLTLTSIAIDRYFVIIYPFHPRMKLSTCIGI 181

Qy        174 TFLIWIVSTLINLPYLMSFE--------------------HVDGSFYVQPG-------- 204

Db        182 IVSIWVIALLATVPYGMYMKMTNELVNGTQTGNETLVEATLMLNGSFVAQGSGFIEAPDS 241

Qy        205 ------------------ETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITYC 246

Db        242 TSATQAYMQVMTAGSTGPEMPYVRVYCEE-NWPSEQYRKVFGAITTTLQFVLPFFIISIC 300

Qy        247 YFKILQKVSKDMIIQNAQFCQSLTQKQRSDA-TSRKKKVNYILIAMVVTFIGCWLPLTLL 305

Db        301 YVWISVKLN-----QRARAKPGSKSSRREEADRDRKKRTNRMLIAMVAVFGLSWLPINVV 355

Qy        306 NLVKDF-KKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWLT---RKQKRSGL----- 356

Db        356 NIFDDFDDKSNEWRFYILFFFV--AHSIAMSSTCYNPFLYAWLNENFRKEFKHVLPCFNP 413

Qy        357 --SKILNSTEGSKKAGGSGLRGIQLH 380

Db        414 SNNNIIINITRGYNRSDRNTC-GPRLH 438


RESULT 6
US-09-721-870-22
; Sequence 22, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Geary, Timothy G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 28341/6223
;  CURRENT APPLICATION NUMBER: US/09/721,870
;  CURRENT FILING DATE:  2000-11-24
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
;   LENGTH: 376
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-721-870-22

  Query Match           24.9%;  Score 515.5;  DB 2;  Length 376;
  Best Local Similarity  30.3%;  Pred. No. 5.2e-35;
  Matches  119;  Conservative   78;  Mismatches  131;  Indels   65;  Gaps   11;

Qy         29 NNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQS 88

Db          2 NGSDCLNLNSELWLYR-EDLSSRWYIMLVFAFLYLIIIAAGIIGNSCVILAITRNKSLQT 60

Qy         89 ARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTA 148

Db         61 VPNLFILSLSCSDIVVCCTSATITPITAFKKEWIFGEALCRIAPFIAGISLCFSTFTLTA 120

Qy        149 ISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFEHVDGSFYVQPGETPY 208

Db        121 ISIDRYILIRFPMRKPITHYQAVGVIAIICAFAATITSPIM--FKQKLGEF------ENF 172

Qy        209 CGHFCDEANW-QSENSRKIYGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQNAQFCQ 267

Db        173 CGQYCTE-NWGANESQRKIYGAALMFLQLVIPLTIIIISYTAISLKIGQSMILKGA---- 227

Qy        268 SLTQKQRSD------------ATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEP 315

Db        228 ---KKQKTDNWEMELSDQQRIAVKRRQRTNRMLIGMVVAFACSWIWSVTFNILRDYEYLP 284

Qy        316 EWLKRQPFFWAINAHVIAMSLVVWNPLLF----------------FWLTRKQKRSG--LS 357

Db        285 ELIKTQEYIFGIATHCIAMTSTVWNPLLYAVLNLQLRAAFIDLMPHWLRRHLNLEGDNSS 344

Qy        358 KILN------STEGSKKAGGSGLRGIQLHDLLP 384

Db        345 PLLNHPTMTITNKPSKQ-----------HTLIP 366


RESULT 7
US-09-721-870-26
; Sequence 26, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Geary, Timothy G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 28341/6223
;  CURRENT APPLICATION NUMBER: US/09/721,870
;  CURRENT FILING DATE:  2000-11-24
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 26
;   LENGTH: 457
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-721-870-26

  Query Match             23.4%;  Score 485.5;  DB 2;  Length 457;
  Best Local Similarity   30.8%;  Pred. No. 2e-32;
  Matches  117;  Conservative   69;  Mismatches  117;  Indels   77;  Gaps   10;

Qy         58 FTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAM 117
              |  :| ||| ||:|||  :::    :| | | :|:|:|||  :| ::   ::|:||   :
Db         29 FLTVYLFLFFLGLFGNVTLIYVTCSHKALLSVQNIFILNLAASDCMMCILSLPITPITNV 88

Qy        118 TKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLI 177
              |:| ||:::|||:|     |:|| ::|| ||:||::: :   |   |:| | |   | |:
Db         89 YKNWYFGNLLCHLIPCIQGISIFVCTFSLGAIALDRYILVVRPHSTPLSQRGAFLTTVLL 148

Qy        178 WIVSTLINLPYLMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFV 237
              ||:| :: |||  : : :: :     |   ||:|| |  |:|  ||: |   ||| |||
Db        149 WILSFVVTLPYAFNMQMIEYT------EERICGYFCTE-KWESAKSRRAYTMIVMLAQFV 201

Qy        238 VPMAVITYCYFKILQKVSK-------DMIIQNA--------------QFCQSLT------ 270
              || ||: :|| |:  :||        |: : :              |:   |
Db        202 VPFAVMAFCYANIVSVLSKRAQTKIRKMVERTSALESSCAFPSHGLEQYENELNEFLDKQ 261

Qy        271 QKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEWLKRQPFF------ 324
              :|::     : ::   ||: ||| |   |||  :::|: ::          | ||
Db        262 EKEKQRVVLQNRRTTSILVTMVVWFGITWLPHNVISLIIEYD------DTQSFFRLYGRD 315

Qy        325 -----WAIN--AHVIAMSLVVWNPLLFFWL----------TRKQKRSGLSKILNST---- 363
                  : :|   | ||||  | ||:|: ||           |    |    :|:| |
Db        316 DYDISYLLNLFTHSIAMSNNVLNPVLYAWLNPSFRQLVIKTYFGDRRKSDRIINQTSVYK 375

Qy        364 ----------EGSKKAGGSG 373
                       |  | || |
Db        376 TKIVHDTKHLNGRAKIGGGG 395


RESULT 8
US-09-721-870-36
; Sequence 36, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Geary, Timothy G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 28341/6223
;  CURRENT APPLICATION NUMBER: US/09/721,870
;  CURRENT FILING DATE:  2000-11-24
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
;   LENGTH: 365
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-721-870-36

  Query Match             22.3%;  Score 461.5;  DB 2;  Length 365;
  Best Local Similarity   30.9%;  Pred. No. 1.6e-30;
  Matches  110;  Conservative   79;  Mismatches  138;  Indels   29;  Gaps    8;

Qy         28 SNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQ 87
              |::  || |  |   |  |:|:     :|   :|  : |:|: ||  |: :| | | ||
Db          2 SSSNHCIDI-RAYLWQTKHDLTLHPIPIAILATIYTIIVVVGVTGNLLVVMSVMRFKVLQ 60

Qy         88 SARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLT 147
              | ||:|:::|  :|: :   :  |||  | :| | ||  :|||:||    ::  :: :||
Db         61 SVRNMFIVSLSVSDIFVAIVSGSVTPITAFSKVWLFGGPLCHLLPLLQGTALSFSTLTLT 120

Qy        148 AISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPY-----LMSFEHVDGSFYVQ 202
              ||::|::: |  |||:|:   ||| :      :|  :::|      || | :
Db        121 AIAIDRYILICHPTKEPIRKDQALKMISFNSAISVGLSVPLFMKQELMQFRN-------- 172

Qy        203 PGETPYCGHFCDEANWQSE-NSRKIYGTTVMLLQFVVPMAVITYCYFKILQKVSKDMIIQ 261
                  |||  :| | ||  :   | :||| | ::||| |:  ||:||  |  |: : : ::
Db        173 -----YCGEYCSE-NWGPDAYLRSVYGTVVFIIQFVFPFLITITFCYASISIKLRRGVFVR 226

Qy        262 NAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEWLKRQ 321
              :|  : |  : |   | |: : | :|| | |||   |||     | ::|:   |  :  |
Db        227 GSQ--KELMSEARRQLTQRRLRTNRMLIIMTVTFALSWLPSVGFNFLRDYSALPGIIDSQ 284

Qy        322 PFFWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKILNSTEGSKKAGGSGLRGI 377
              : : |  | |:|: |: || |: :   :  |:  : :|:: : :      |:| :
Db        285 DYLFGIIFHCISMTSVIVNPFLYGY-CNEHFRAAFAALLDTVKAA-----CGMRRV 334


RESULT 9
US-09-721-870-14
; Sequence 14, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Geary, Timothy G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 28341/6223
;  CURRENT APPLICATION NUMBER: US/09/721,870
;  CURRENT FILING DATE:  2000-11-24
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-721-870-14

  Query Match             22.2%;  Score 460.5;  DB 2;  Length 387;
  Best Local Similarity   28.5%;  Pred. No. 2e-30;
  Matches  105;  Conservative   80;  Mismatches  118;  Indels   65;  Gaps    8;

Qy         47 DITVDFYIRSIFTFLYGFLFVLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVF 106
              |:| :  :   |: ||  :|:||| ||  ||:  ::::||: :|:|:|||  :::::
Db         18 DMTNEPTVLVTFSLLYLHIFLLGILGNSAVLYLTMKHRQLQTVQNIFILNLCASNVLMCL 77

Qy        107 TAIPVTPWYAMTKDWAFGSVMCHLVPLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVS 166
              |:|:|     : | | | | :| |:|     |:||:::||:||:||::  :  | || :|
Db         78 TSLPITPITNVYKQWFFSSPVCKLIPLVQGASIFVSTFSLSAIALDRYNLVVRPHKQKLS 137

Qy        167 IRQALAITFLIWIVSTLINLPY--LMSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSR 224
              | |: |  |||::| :: :||   |  | ::|              || :| | :|      |
Db        138 SRSAMMIALLIWVISVVVCMPYGWYMDVEKLNG----------LCGEYCSE-HWPLAEVR 186

Qy        225 KIYGTTVMLLQFVVPMAVITYCYFKI-----------LQKVS-KDMIIQNAQFC------ 266
              | |    |:: ||: | | : :||: |           |:|:| :  :::|:  |
Db        187 KGYTFLVLITQFLPFFATMAFCYYNIFSRLRQRVETKLKKLSERSQLLENSTTCGTTNHI 246

Qy        267 ---------QSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFKKEPEW 317
                      |  |||    :::::   ||  ||: |   |||  :: |: ::
Db        247 VSINAEAVQNGLENKQRLAVLAQQRRTTTILSCMVLLFAFTWLPHNVVTLMIEY------ 300

Qy        318 LKRQPFFW----------------AINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKILN 361
                 ||:                 :: ||:|:|   | || |: ||    |   :  :
Db        301 ---DGFFFHSDETSATSTDHTYIVSMTAHLISMLTNVTNPFLYAWLNPMFKEMLIKTLRG 357

Qy        362 STEGSKKA 369
               ::  | |
Db        358 GSKSPKPA 365


RESULT 10
US-09-721-870-12
; Sequence 12, Application US/09721870
```

```
; Patent No. 6632621
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Geary, Timothy G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 28341/6223
;  CURRENT APPLICATION NUMBER: US/09/721,870
;  CURRENT FILING DATE:  2000-11-24
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 381
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-721-870-12

  Query Match             22.1%;  Score 458;  DB 2;  Length 381;
  Best Local Similarity   30.5%;  Pred. No. 3.2e-30;
  Matches  108;  Conservative   77;  Mismatches  109;  Indels   60;  Gaps   12;

Qy          7 TISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLF 66
              ::|:|   ||||  |       ||   ::                  | |  |  :|  :|
Db          8 SVSSILNETTPSYQST--CKIKNNPMEME----------------YFRPFFISMYCAVF 48

Qy         67 VLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSV 126
              ::   ||  |:: |  |||:|:  |:|: ||  :|::: ||:: :|| |      | ||
Db         49 LVASSGNFLVVYVVMTNKRMQTITNIFITNLAVSDIMVNFTSLWLTPTYTSIGHWIFGGG 108

Qy        127 MCHLVPLSNSCSVFVTSWSLTAISLDKF---------LHINDPTKQPVSIRQALAITFLI 177
              :|| :||    |:|:::|:||||::|::         ::|||     :|:|  |:   ||
Db        109 LCHGLPLFQGTSIFISTWTLTAIAIDRYIVIVHNSSNININD----RMSMRSCLSFIVLI 164

Qy        178 WIVSTLINLPYL----MSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVML 233
              |: | |:  ||     ::: |    | :           | | :| :   | |:|  ||:
Db        165 WLCSLLLVTPYAINMKLNYIHEPCDFLI----------CSE-DWSNAEFRSIFGIVVMI 212

Qy        234 LQFVVPMAVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVV 293
              |||::|  :|   | ||        :  |::  ||:|:: :||   |||::  :|| |||
Db        213 LQFILPFVLIAISYIKI-------WLFLNSR--QSMTER-KSD-IKRKKRLLRMLIVMVV 261

Qy        294 TFIGCWLPLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWL 347
              |  || |  ||| ::| | :  :::    |  :: |:::|:   |||:|: ::
Db        262 IFAICWFPFNLLNCLRDLKLD-NFMRGYFSFVFLSVHLMSMTATAWNPILYAFM 314


RESULT 11
US-09-721-870-8
; Sequence 8, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Geary, Timothy G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 28341/6223
;  CURRENT APPLICATION NUMBER: US/09/721,870
;  CURRENT FILING DATE:  2000-11-24
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 402
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-721-870-8

  Query Match             22.1%;  Score 458;  DB 2;  Length 402;
  Best Local Similarity   30.5%;  Pred. No. 3.4e-30;
  Matches  108;  Conservative   77;  Mismatches  109;  Indels   60;  Gaps   12;

Qy          7 TISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLF 66
              ::|:|   ||||  |       ||   ::                  | |  |  :|  :|
Db          8 SVSSILNETTPSYQST--CKIKNNPMEME----------------YFRPFFISMYCAVF 48

Qy         67 VLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSV 126
              ::   ||  |:: |  |||:|:  |:|: ||  :|::: ||:: :|| |      | ||
Db         49 LVASSGNFLVVYVVMTNKRMQTITNIFITNLAVSDIMVNFTSLWLTPTYTSIGHWIFGGG 108

Qy        127 MCHLVPLSNSCSVFVTSWSLTAISLDKF---------LHINDPTKQPVSIRQALAITFLI 177
              :|| :||    |:|:::|:||||::|::         ::|||     :|:|  |:   ||
Db        109 LCHGLPLFQGTSIFISTWTLTAIAIDRYIVIVHNSSNININD----RMSMRSCLSFIVLI 164

Qy        178 WIVSTLINLPYL----MSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVML 233
              |: | |:  ||     ::: |    | :           | | :| :   | |:|  ||:
Db        165 WLCSLLLVTPYAINMKLNYIHEPCDFLI----------CSE-DWSNAEFRSIFGIVVMI 212

Qy        234 LQFVVPMAVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVV 293
              |||::|  :|   | ||        :  |::  ||:|:: :||   |||::  :|| |||
Db        213 LQFILPFVLIAISYIKI-------WLFLNSR--QSMTER-KSD-IKRKKRLLRMLIVMVV 261

Qy        294 TFIGCWLPLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWL 347
              |  || |  ||| ::| | :  :::    |  :: |:::|:   |||:|: ::
Db        262 IFAICWFPFNLLNCLRDLKLD-NFMRGYFSFVFLSVHLMSMTATAWNPILYAFM 314


RESULT 12
US-09-721-870-6
; Sequence 6, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Geary, Timothy G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 28341/6223
;  CURRENT APPLICATION NUMBER: US/09/721,870
;  CURRENT FILING DATE:  2000-11-24
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 404
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-721-870-6

  Query Match             22.1%;  Score 458;  DB 2;  Length 404;
  Best Local Similarity   30.5%;  Pred. No. 3.5e-30;
  Matches  108;  Conservative   77;  Mismatches  109;  Indels   60;  Gaps   12;

Qy          7 TISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLF 66
              ::|:|   ||||  |       ||   ::                  | |  |  :|  :|
Db          8 SVSSILNETTPSYQST--CKIKNNPMEME----------------YFRPFFISMYCAVF 48

Qy         67 VLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSV 126
              ::   ||  |:: |  |||:|:  |:|: ||  :|::: ||:: :|| |      | ||
Db         49 LVASSGNFLVVYVVMTNKRMQTITNIFITNLAVSDIMVNFTSLWLTPTYTSIGHWIFGGG 108

Qy        127 MCHLVPLSNSCSVFVTSWSLTAISLDKF---------LHINDPTKQPVSIRQALAITFLI 177
              :|| :||    |:|:::|:||||::|::         ::|||     :|:|  |:   ||
Db        109 LCHGLPLFQGTSIFISTWTLTAIAIDRYIVIVHNSSNININD----RMSMRSCLSFIVLI 164

Qy        178 WIVSTLINLPYL----MSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVML 233
              |: | |:  ||     ::: |    | :           | | :| :   | |:|  ||:
Db        165 WLCSLLLVTPYAINMKLNYIHEPCDFLI----------CSE-DWSNAEFRSIFGIVVMI 212

Qy        234 LQFVVPMAVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVV 293
              |||::|  :|   | ||        :  |::  ||:|:: :||   |||::  :|| |||
Db        213 LQFILPFVLIAISYIKI-------WLFLNSR--QSMTER-KSD-IKRKKRLLRMLIVMVV 261

Qy        294 TFIGCWLPLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWL 347
              |  || |  ||| ::| | :  :::    |  :: |:::|:   |||:|: ::
Db        262 IFAICWFPFNLLNCLRDLKLD-NFMRGYFSFVFLSVHLMSMTATAWNPILYAFM 314
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RESULT 13
US-09-721-870-10
; Sequence 10, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Geary, Timothy G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 28341/6223
;  CURRENT APPLICATION NUMBER: US/09/721,870
;  CURRENT FILING DATE:  2000-11-24
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 406
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-721-870-10

  Query Match             22.1%;  Score 458;  DB 2;  Length 406;
  Best Local Similarity   30.5%;  Pred. No. 3.5e-30;
  Matches  108;  Conservative   77;  Mismatches  109;  Indels   60;  Gaps   12;

Qy          7 TISTISTTTTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLF 66
              ::|:|   ||||  |       ||  ::                  | |  | :|  :|
Db          8 SVSSILNETTPSYQST--CKIKNNPMEME----------------YFRPFFISMYCAVF 48

Qy         67 VLGIFGNGGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFGSV 126
              ::   ||  |:: |  |||:|:  |:|: ||  :|::: ||:: :|| |      | ||
Db         49 LVASSGNFLVVYVVMTNKRMQTITNIFITNLAVSDIMVNFTSLWLTPTYTSIGHWIPGGG 108

Qy        127 MCHLVPLSNSCSVFVTSWSLTAISLDKF---------LHINDPTKQPVSIRQALAITFLI 177
              :|| :||    |:|:::|:||||::|::         ::|||     :|:|  |:   ||
Db        109 LCHGLPLFQGTSIFISTWTLTAIAIDRYIVIVHNSSNININD----RMSMRSCLSFIVLI 164

Qy        178 WIVSTLINLPYL----MSFEHVDGSFYVQPGETPYCGHFCDEANWQSENSRKIYGTTVML 233
              |: | |:  ||      ::: |    | :            | | :| :   | |:|  ||:
Db        165 WLCSLLLVTPYAINMKLNYIHEPCDFLI----------CSE-DWSNAEFRSIFGIVVMI 212

Qy        234 LQFVVPMAVITYCYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVV 293
              |||::|  :|   | ||          :  |::  ||:|:: :||   |||::  :|| |||
Db        213 LQFILPFVLIAISYIKI-------WLFLNSR--QSMTER-KSD-IKRKKRLLRMLIVMVV 261

Qy        294 TFIGCWLPLTLLNLVKDFKKEPEWLKRQPFFWAINAHVIAMSLVVWNPLLFFWL 347
              |  || |  ||| ::| | :  :::    |  :: |:::|:   |||:|: ::
Db        262 IFAICWFPFNLLNCLRDLKLD-NFMRGYFSFVFLSVHLMSMTATAWNPILYAFM 314


RESULT 14
US-09-693-746-6
; Sequence 6, Application US/09693746
; Patent No. 6835546
; GENERAL INFORMATION:
;  APPLICANT: Lowery, David E.
;  APPLICANT:  Smith, Valdin G.
;  APPLICANT:  Kubiak, Teresa M.
;  APPLICANT:  Larsen, Martha J.
;  TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
;  TITLE OF INVENTION:  Related To The Same
;  FILE REFERENCE: 6297.1cp
;  CURRENT APPLICATION NUMBER: US/09/693,746
;  CURRENT FILING DATE:  2000-10-20
;  PRIOR APPLICATION NUMBER: 09/425,676
;  PRIOR FILING DATE: 1999-10-22
;  NUMBER OF SEQ ID NOS: 168
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 458
;   TYPE: PRT
;   ORGANISM: D. melanogaster
US-09-693-746-6

  Query Match             18.7%;  Score 388;  DB 2;  Length 458;
  Best Local Similarity   27.7%;  Pred. No. 2.7e-24;
  Matches  112;  Conservative   79;  Mismatches  157;  Indels   56;  Gaps   15;

Qy         25 TSHSNNGSCIQIAE--AIAAQGIDDITVDFYIRS---------IFTFLYGFLFVLGIFGN 73
              | |: | : |  ::     :: :| : :| :: :          :   :|| | | |  ||
Db         41 TVHALNTTAINTSDLNETGSRPLDPVLIDRFLSNRAVDSPWYHMLISMYGVLIVFGALGN 100

Qy         74 GGVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAMTKDWAFG--SVMCHLV 131
               |: || |   :::|||:|:|||  :||:|    :|:|    ::| | :|  |::|  :
Db        101 TLVVIAVIRKPIMRTARNLFILNLAISDLLLCLVTMPLTLMEILSKYWPYGSCSILCKTI 160

Qy        132 PLSNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMS 191
               :  :  :||:: |:|||: |::  |  ||:  :    |: |   || :: |:  |  :
Db        161 AMLQALCIFVSTISITAIAFDRYQVIVYPTRDSLQFVGAVTILAGIWALALLLASPLFVY 220

Qy        192 FE--HVDGSFYVQ----PGETPYCGHFCDEANWQSENSRKIYGTTVMLLQFVVPMAVITY 245
               |  : |    :|         |||        :| | | |    : :|::||: :::
Db        221 KELINTDTPALLQQIGLQDTIPYC-----IEDWPSRNGRFYYSIFSLCVQYLVPILIVSV 275

Qy        246 CYFKILQKVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLL 305
               || |  |:   : :   |   :  : :|     | |: | :||:: : |   ||||
Db        276 AYFGIYNKLKSRITVVAVQASSAQRKVERG---RRMKRTNCLLISIAIIFGVSWLPLNFF 332

Qy        306 NLVKDFKKEP---EWLKRQPFFWAINAHVIAMSLVVWNPLLFFWL----------TRKQ 351
              ||  | :: |     | |    :||  |:| ||    ||||: ||          ||:
Db        333 NLYADMERSPVTQSMLVR----YAI-CHMIGMSSACSNPLLYGWLNDNFRCNVQAAARKR 387

Qy        352 KRSGLS------KILN-STEGSKKAGGSGLRGIQLHDLLPTSTH 388
              :: |        |:|      |  ||| |  |:   | : |  |
Db        388 RKLGAELSKGELKLLGPGGAQSGTAGGEG--GLAATDFM-TGHH 428


RESULT 15
US-08-513-974B-26
; Sequence 26, Application US/08513974B
; Patent No. 6114139
;  GENERAL INFORMATION:
;    APPLICANT:  Hinuma, Shuji
;    APPLICANT:  Hosoya, Masaki
;    APPLICANT:  Fujii, Ryo
;    APPLICANT:  Ohtaki, Tetsuya
;    APPLICANT:  Fukusumi, Shoji
;    APPLICANT:  Ohgi, Kazuhiro
;    TITLE OF INVENTION:  G PROTEIN COUPLED RECEPTOR PROTEIN,
;    TITLE OF INVENTION:  PRODUCTION, AND USE THEREOF
;    NUMBER OF SEQUENCES:  380
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/513,974B
;      FILING DATE:  14-SEP-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP95/01599
;      FILING DATE:  10-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-093989
;      FILING DATE:  19-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-057186
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;      FILING DATE:  16-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-007177
;      FILING DATE:  20-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-326611
;      FILING DATE:  28-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-270017
;      FILING DATE:  02-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-236357
;      FILING DATE:  30-SEP-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-236356
;      FILING DATE:  30-SEP-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-189274
;      FILING DATE:  11-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-189273
;      FILING DATE:  11-AUG-1945
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-189272
;      FILING DATE:  11-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Resnick, David S.
;      REGISTRATION NUMBER:  34,235
;      REFERENCE/DOCKET NUMBER:  45753
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  370 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-513-974B-26

  Query Match             18.6%;  Score 386;  DB 2;  Length 370;
  Best Local Similarity   27.5%;  Pred. No. 3.1e-24;
  Matches   96;  Conservative   83;  Mismatches  146;  Indels   24;  Gaps   10;

Qy         15 TTPSTISNVITSHSNNGSCIQIAEAIAAQGIDDITVDFYIRSIFTFLYGFLFVLGIFGNG 74
              |||:  |    : : ||| :  |:| |       : :   :: :   ||  : |:|: ||
Db         23 TTPANQS--AEASAGNGS-VAGADAPAVTPFQSLQLVHQLKGLIVLLYSVVVVVGLVGNC 79

Qy         75 GVLWAVARNKRLQSARNVFLLNLIFTDLILVFTAIPVTPWYAM-TKDWAFGSVMCHLVPL 133
               ::  :|| :|| :  |  : ||  :|:::    :|:|  ||   : | ||  :||||
Db         80 LLVLVIARVRRLHNVTNFLIGNLALSDVLMCTACVPLTLAYAFEPRGWVFGGGLCHLVFF 139

Qy        134 SNSCSVFVTSWSLTAISLDKFLHINDPTKQPVSIRQALAITFLIWIVSTLINLPYLMSFE 193
              :|:|: ::|| |::|::: :  | :: :|:| :      || :| :: ||  :
Db        140 LQPVTVYVSVFTLTTIAVDRYVVLVHPLRRRISLRLSAYAVLAIWALSAVLALPAAVHTY 199

Qy        194 HVDGSFYVQPGETPYCGHFCDEANWQS-ENSRKIYGTTVMLLQFVVPMAVITYCYFKILQ 252
              ||:    ::| :   |  |     | | |  |::|   ::|: :::|: ||   | ::
Db        200 HVE----LKPHDVRLCEEF-----WGSQERQRQLYAWGLLLVTYLLPLLVILLSYVRVSV 250

Qy        253 KVSKDMIIQNAQFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGCWLPLTLLNLVKDFK 312
              |      ::|      :|| |     :|:::   :|: :|| |  ||||| : ||::|
Db        251 K------LRNRVVPGCVTQSQADWDRARRRRTFCLLVVVVVVFAVCWLPLHVFNLLRDL- 303

Qy        313 KEPEWLKRQPF-FWAINAHVIAMSLVVWNPLLFFWLTRKQKRSGLSKIL 360
             :|  :    |    :  | :|||   :|| :: ||      |  | |:|
Db        304 -DPHAIDPYAFGLVQLLCHWLAMSSACYNPFIYAWL-HDSFREELRKLL 350


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Job time : 49 secs
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